

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: August 17, 2002, 00:36:05 ; Search time 24.74 Seconds
(without alignments)

400.655 Million cell updates/sec

Title: US-09-824-134-2

Perfect score: 1302

Sequence: 1 VQAPECRFGGILGLPKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	79.9	208	1	FADD_HUMAN
2	719.5	55.3	205	1	FADD_MOUSE
3	122	9.4	479	1	ICB8_HUMAN
4	121.5	9.3	1880	1	ANK1_HUMAN
5	117.5	9.0	1862	1	ANK1_MOUSE
6	115.5	8.9	656	1	RIP_MOUSE
7	111.5	8.6	671	1	RIP_HUMAN
8	110	8.4	480	1	CFLA_HUMAN
9	108	8.3	521	1	ICB2_HUMAN
10	99	7.6	3924	1	ANK2_HUMAN
11	98.5	7.6	4644	1	DYHC_MOUSE
12	98.5	7.6	4844	1	DYHC_RAT
13	96.5	7.4	535	1	HTR1_HALSA
14	95.5	7.3	497	1	RP54_PSEAE
15	93.5	7.2	324	1	TNR6_RAT
16	91.5	7.0	470	1	ARYL_MYCTU
17	91.5	7.0	1816	1	LMA4_HUMAN
18	91	7.0	3695	1	LMA5_HUMAN
19	90.5	7.0	130	1	PE15_MOUSE
20	90.5	7.0	411	1	KICL_RABIT
21	90	6.9	295	1	X769_HUMAN
22	90	6.9	953	1	Y442_HUMAN
23	89.5	6.9	535	1	HPL1_HALNI
24	89.5	6.9	962	1	ARVC_MOUSE
25	89	6.8	483	1	KICL_MOUSE
26	88.5	6.8	130	1	PE15_HUMAN
27	88.5	6.8	892	1	AAAC1_HUMAN
28	88.5	6.8	893	1	AAAC1_CHICK
29	87.5	6.7	433	1	CGBL_HUMAN
30	87.5	6.7	484	1	CFLA_MOUSE
31	87.5	6.7	894	1	CFLA_MOUSE
32	87.5	6.7	3433	1	UTRO_HUMAN
33	87	6.7	332	1	TNR6_PIG

34	86.5	6.6	294	1	PARB_CAUCR
35	86.5	6.6	1073	1	MTR4_YEAST
36	86	6.6	587	1	YCAQ_HAEIN
37	86	6.6	1453	1	Y373_BOVIN
38	85.5	6.6	880	1	RASO_PYRAB
39	85	6.5	899	1	PLC1_SCHPO
40	84.5	6.5	892	1	AAAC1_RAT
41	84.5	6.5	903	1	YB56_METJA
42	84	6.5	209	1	TRIC_HUMAN
43	84	6.5	1957	1	YD86_SCHPO
44	83.5	6.4	171	1	CFLA_HSV2
45	83.5	6.4	283	1	LECH_MOUSE

ALIGNMENTS

RESULT 1
FADD_HUMAN STANDARD; PRT; 208 AA.
AC Q13158; Q14866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FADD protein (FAS-associating death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN FADD OR MORT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC TISSUE-Umbilical vein endothelial cells;
RX MEDLINE=95277837; PubMed=7538907;
RA Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
RT "FADD, a novel death domain-containing protein, interacts with the
RT death domain of Fas and initiates apoptosis.";
RL Cell 81:505-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95229578; PubMed=7536190;
RA Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
RA Wallach D.;
RT "A novel protein that interacts with the death domain of Fas/AP01
RT contains a sequence motif related to the death domain.";
RL J. Biol. Chem. 270:7795-7798(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RN [4]
RP Submitted (NOV-2000) to the EMBL/GenBank/DBAJ databases.
RT STRUCTURE BY NMR OF 1-83.
RX MEDLINE=98241233; PubMed=9582077;
RA Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
RA Lenardo M.J., Fesik S.W.;
RT "NMR structure and mutagenesis of the FADD (Mort1) death-effector
RT domain.";
RL Nature 392:941-945(1998).
CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS.
CC -1- SUBUNIT: INTERACTS WITH CFLAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT
CC FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

O05190 caulobacter
P47047 saccharomyc
P44144 haemophilus
O9tu23 bos taurus
Q9uzc8 pyrococcus
P49977 schizosacch
Q921p2 rattus norv
Q58556 methanococc
P19429 homo sapien
O10411 schizosacch
Q66674 equine herp
P34927 mus musculu

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 CC or send an email to license@isb-sib.ch).

DR EMBL; U24231; AAA86517.1;
 DR EMBL; X84709; CAA59197.1;
 DR EMBL; BC000334; AAH00334.1;
 DR PDB; 1A1W; 16-FEB-99.
 DR PDB; 1A1Z; 16-FEB-99.
 DR MIM; 602457;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PS50168; DED; 1.
 DR PROSITE; PS50168; DED; 1.
 DR Apoptosis; 3D-structure.
 DR DOMAIN 3 81
 DR MUTAGEN 97 181
 DR MUTAGEN 121 121
 DR CONFLICT 32 32 G -> V (IN REF. 2).
 DR SEQUENCE 208 AA; 23279 MW; 065E2F852E83507 CRC64;

Query Match 79.9%; Score 1040; DB 1; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.2e-74;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTEKFLCGRVVKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTEKFLCGRVVKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDICAAFNVICDNVGDWRRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDICAAFNVICDNVGDWRRLAROLK 120
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 2
 FADD_MOUSE
 ID FADD_MOUSE STANDARD; PRT; 205 AA.
 AC Q61160; Q61082;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FADD protein (FAS-associated death domain-containing protein)
 GN (Mediator of receptor induced toxicity).
 GN FADD OR MORT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96220459; PubMed-8649383;
 RA Zhang J., Winoto A.;
 RT "A mouse Fas-associated protein with homology to the human MORT1/FADD
 RL protein is essential for Fas-induced apoptosis.",
 Mol. Cell. Biol. 16:2756-2763(1996).

RP SEQUENCE FROM N.A.
 RX MEDLINE-96152659; PubMed-8565075;
 RA Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
 RT "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
 RL receptor 1 signal transduction pathways.",
 Cell 84:299-308(1996).
 CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
 CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
 CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
 CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
 CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
 CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
 CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
 CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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DR EMBL; U50406; AAB07789.1;
 DR EMBL; U43184; AAA97876.1;
 DR HSP; Q13158; IALZ.
 DR MGD; MGI-109324; Fadd.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50168; DED; 1.
 KW Apoptosis.
 FT DOMAIN 3 81
 FT DOMAIN 97 181
 FT CONFLICT 168 168
 FT SEQUENCE 205 AA; 22960 MW; 4BC8D86B33A58783 CRC64;

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

QY 49 MDPLVLLHSVSSSSSELTEKFLCGRVVKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTEKFLCGRVVKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDICAAFNVICDNVGDWRRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDICAAFNVICDNVGDWRRLAROLK 120
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSEAKMDIEEKYPRSLSERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 DB 181 QES---VSKSENMPVLRDSTVSSE 203

RESULT 3
 ICEB_HUMAN
 ID ICEB_HUMAN STANDARD; PRT; 479 AA.
 AC Q14790; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;
 AC Q15806; Q9UQ81; Q14676;
 DT 01-NOV-1997 (Rel. 35, Created)

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 00:37:50 ; Search time 2174.44 Seconds
(without alignments)
16370.210 Million cell updates/sec

Title: US-09-824-134-1
Perfect score: 1701
Sequence: 1 GTGAATCAGGACCGAGTG.....ACAAAAA.....1701

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

RESULT	1	1701	100.0	1701	9	HSMRINTX
LOCUS	HSMRINTX	1672.8	98.3	1734	9	BC000334
DEFINITION	H. sapiens mRNA for mediator of receptor-induced toxicity.	1621.8	95.3	1642	9	HSU24231
ACCESSION	X84709	1326.4	78.0	1642	9	HSU74301
VERSION	X84709.1	1247.4	73.3	169725	9	AP000879
KEYWORDS	MORT1 gene.	728	43.4	143409	2	AP001787
SOURCE	human	439	27.0	78291	2	AC023216
ORGANISM	Homo sapiens	427	25.1	1634	9	HSU62022
REFERENCE		365.6	21.5	1512	10	BC004584
AUTHORS		365.6	21.5	1512	10	BC021400
TITLE		363.8	21.4	1377	10	MMU50406
JOURNAL		359	21.1	618	10	MMU43184
MEDLINE		341	20.0	143409	2	AP001787
REFERENCE		312.6	18.4	66127	2	AC067995
AUTHORS		288.8	17.0	298	6	AX138456
TITLE		62.2	3.7	39524	1	SCN10
JOURNAL		62	3.6	125020	9	AF429315
MEDLINE		59.2	3.5	200050	1	AL646068
REFERENCE		58.6	3.4	216050	1	SCE34
AUTHORS		57.8	3.4	2497	1	RSHEMZFN
TITLE		57.2	3.4	53184	2	AC110059
JOURNAL		56.8	3.4	158174	8	AP003414
MEDLINE		56.8	3.3	10948	1	AE005746
REFERENCE		56.6	3.3	171977	2	AC080022
AUTHORS		56.4	3.3	11886	1	AE004638
TITLE		56.2	3.3	125020	9	AF429315
JOURNAL		55.6	3.3	143278	2	OSJN00087
MEDLINE		55.6	3.3	24808	2	AC104312
REFERENCE		55.6	3.3	33820	1	SCE20
AUTHORS		54.8	3.2	18270	1	AF148496
TITLE		54.6	3.2	151773	8	AP001551
JOURNAL		54.4	3.2	150594	8	AP001859
MEDLINE		54.2	3.2	207683	2	AC098712
REFERENCE		53.8	3.2	4573	1	AB056583
AUTHORS		53.6	3.2	12249	1	AE004632
TITLE		53.6	3.2	108705	2	AP004182
JOURNAL		53.6	3.2	115154	2	AP003804
MEDLINE		52.8	3.2	272545	2	AC090533
REFERENCE		52.6	3.1	11059	14	PRVULGNS
AUTHORS		52.6	3.1	33084	1	SC8E4A
TITLE		52.6	3.1	39207	1	SC4G1
JOURNAL		52.6	3.1	68750	1	AF210843
MEDLINE		52.6	3.1	105965	2	AC108986
REFERENCE		52.6	3.1	175296	2	AC106674

ALIGNMENTS

RESULT 1
LOCUS HSMRINTX 1701 bp mRNA linear PRI 27-APR-1995
DEFINITION H. sapiens mRNA for mediator of receptor-induced toxicity.
ACCESSION X84709
VERSION X84709.1 GI:791037
KEYWORDS MORT1 gene.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1701)
Boldin, M.P., Varfolomeev, E.E., Pancer, Z., Mett, I.L., Camonis, J.H.
and Wallach, D.
A novel protein that interacts with the death domain of Fas/AP01
contains a sequence motif related to the death domain
J. Biol. Chem. 270 (14), 7795-7798 (1995)
9529578
2 (bases 1 to 1701)
Wallach, D.,
Direct Submission
Submitted (10-FEB-1995) D. Wallach, The Weizmann Institute, Dept of
Membrane Research & Biophysics, Rehovot 76100, ISRAEL

FEATURES

source Location/Qualifiers
 1. .1701
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="human monocyte, HeLa"
 145..771
 /gene="MORT1"
 145..771
 /gene="MORT1"
 /note="putative start point"
 /codon_start=1
 /product="mediator of receptor induced toxicity"
 /protein_id="CAA59197.1"
 /db_xref="gi:791038"
 /translation="MDPLVLLHSVSSLSSELTELKFLCIRVVKRLERVQSGLD
 LFSMLLEQNDLEPCHTELLRELLASLRHDLRLRRVDFEAGAAGAAPGEEDLCAAFN
 VICDNVGDNRRLARQLKVSDDTKIDSDIEDYPRNLTFERVESLRINKTEKENATVAH
 LVGALRSCQNLVADLVQEVQOARDLQNRSGAMSPMSWNSDASTSEAS"
 E COUNT 382 a 459 c 517 g 343 t
 ORIGIN

Query Match 100.0%; Score 1701; DB 9; Length 1701;
 Best Local Similarity 100.0%; Pred. No. 5.7e-277;
 Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAATCAGGCACCGGAGTGCAGGTTCGGGGTGGAAATCCTTGGGCGCGCTGGCAACGG 60
 Db 1 GTGAATCAGGCACCGGAGTGCAGGTTCGGGGTGGAAATCCTTGGGCGCGCTGGCAACGG 60

Qy 61 CGAGACCTGGCCAGGCGCAGGACGCGAGGACAGAGGCGCGGAGGCGCGGCGCGAG 120
 Db 61 CGAGACCTGGCCAGGCGCAGGACGCGAGGACAGAGGCGCGGAGGCGCGGCGCGAG 120

Qy 121 CCCGGCGCGCTTGAGACCCCGCATGACCCGTTCTGTGCTGCTGCTGCTGCTGCTGCTG 180
 Db 121 CCCGGCGCGCTTGAGACCCCGCATGACCCGTTCTGTGCTGCTGCTGCTGCTGCTGCTG 180

Qy 181 TCCAGCTGTGAGCAGGAGCTGACCGAGTCAAGTTCCTATGCTGCTGCGGCGCGTGGTC 240
 Db 181 TCCAGCTGTGAGCAGGAGCTGACCGAGTCAAGTTCCTATGCTGCTGCGGCGCGTGGTC 240

Qy 241 AAGCGCAAGCTGGAGCGCTGACAGCGGCTAGACCTCTCTCCATCTCTCTGCTGCTGAGCAG 300
 Db 241 AAGCGCAAGCTGGAGCGCTGACAGCGGCTAGACCTCTCTCCATCTCTCTGCTGCTGAGCAG 300

Qy 301 AACGACCTGGAGCCCGGACACCGAGCTCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTG 360
 Db 301 AACGACCTGGAGCCCGGACACCGAGCTCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTG 360

Qy 361 CACGACCTGCTGCGGCGCTGCGAGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGCT 420
 Db 361 CACGACCTGCTGCGGCGCTGCGAGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGCT 420

Qy 421 GGGGAAGAAGACCTGTGTGAGCATTAAAGTTCATATGTATATGTATATGTATATGTATAT 480
 Db 421 GGGGAAGAAGACCTGTGTGAGCATTAAAGTTCATATGTATATGTATATGTATATGTATAT 480

Qy 481 AGAAGGCTGCTGTGAGCTCAAGTCTCAGACCAAGATCAGACATCAGGACAGAG 540
 Db 481 AGAAGGCTGCTGTGAGCTCAAGTCTCAGACCAAGATCAGACATCAGGACAGAG 540

Qy 541 TACCCCGCAACCTGACAGAGCTGTGCGGAGTCACTGAGATCTGGAAGAACACAGAG 600
 Db 541 TACCCCGCAACCTGACAGAGCTGTGCGGAGTCACTGAGATCTGGAAGAACACAGAG 600

Qy 601 AAGGAGAACCAACAGTGGCGCCACCTGGTGGGGCTCTCAGGCTCTGCGAGATGAACCTG 660
 Db 601 AAGGAGAACCAACAGTGGCGCCACCTGGTGGGGCTCTCAGGCTCTGCGAGATGAACCTG 660

Qy 661 GTGGCTGACCTGTACAGAGTTTACAGAGCCCGTGCCTCCAGAACAGGAGTGGGGCC 720
 Db 661 GTGGCTGACCTGTACAGAGTTTACAGAGCCCGTGCCTCCAGAACAGGAGTGGGGCC 720

Db	907	TATTAATGCTCTCCCGCACCAGCGGCTTGGCCCTGCACAGATATTTCCATTTCTT	1966
Qy	982	CCTCACTATGACACTGACAGATCTTGTCTCCACTAAATGAGCTCCTGGGGAGTAGTT	1041
Db	967	CCTCACTATGACACTGACAGATCTTGTCTCCACTAAATGAGCTCCTGGGGAGTAGTT	1026
Qy	1042	GGAAAGTTGGAAACCGTGTCCAGCAGAGAGAAATCTGTCAGATGACACTCACACTGTT	1101
Db	1027	GGAAAGTTGGAAACCGTGTCCAGCAGAGAGAAATCTGTCAGATGACACTCACACTGTT	1086
Qy	1102	ACTCCACAGCGGAGGACACAGCTCAGAGCCAGGATCGGAGGAGGAGGAGGAGGAGG	1161
Db	1087	ACTCCACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1146
Qy	1162	AGAACTGGGATTTGAACCCCGGCGCATCTTCACAGAGCCATGCTCAACACTGTGGG	1221
Db	1147	AGAACTGGGATTTGAACCCCGGCGCATCTTCACAGAGCCATGCTCAACACTGTGGG	1206
Qy	1222	TTCTGCTGCCCTGCGAGTTGGCAGAAAGGATGTTTTTGTCCCATTTCTTGGAGGCCACC	1281
Db	1207	TTCTGCTGCCCTGCGAGTTGGCAGAAAGGATG-TTTTGTCCCATTTCTTGGAGGCCACC	1265
Qy	1282	GGGACAGACTGGACACTAGGGTCAGCGGGGTGCTGTGGTGGGAGGAGGAGGAGGAGG	1341
Db	1266	GGGACAGACTGGACACTAGGGTCAGCGGGGTGCTGTGGTGGGAGGAGGAGGAGGAGG	1325
Qy	1342	GTGGGGTGGGAGAGCTGTTGGCGGTGCTGAGCTCTTGGCGGCTGCTGCTGCTGCTGCTG	1401
Db	1326	GTGGGGTGGGAGAGCTGTTGGCGGTGCTGAGCTCTTGGCGGCTGCTGCTGCTGCTGCTG	1385
Qy	1402	CTCTCTCTGAGACTGCTAAAGTAGGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1461
Db	1386	CTCTCTCTGAGACTGCTAAAGTAGGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1445
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VERSION	U74301.1		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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JOURNAL	Kim, P. K. M., Dutra, A., Chandrasekharappa, S. C. and Puck, J. M.		
REFERENCE	Genomic structure and mapping of human FADD, an intracellular		
AUTHORS	mediator of lymphocyte apoptosis		
TITLE	J. Immunol. (1996) In press		
JOURNAL	2 (bases 1 to 1642)		
AUTHORS	Kim, P. K. and Puck, J. M.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-OCT-1996) LGT, NCHCR, NIH, RM 3B07 Bldg. 49, 49		

FEATURES
source

Convent Dr., Bethesda, MD 20892-4442, USA
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run On: August 17, 2002, 00:37:50 ; Search time 2174.44 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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MEDLINE						
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JOURNAL						

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U24231 Human Fas-a
U74301 Human FADD
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H.sapiens mRNA for mediator of receptor-induced toxicity.

X84709.1 GI:791037

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human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1701)

Boldin,M.P., Varfolomeev,E.E., Pancer,Z., Mett,I.L., Camonis,J.H.

A novel protein that interacts with the death domain of Fas/APO1

contains a sequence motif related to the death domain

J. Biol. Chem. 270 (14), 7795-7798 (1995)

95229578

2 (bases 1 to 1701)

Wallach,D.,
Submitted (10-FEB-1995) D. Wallach, The Weizmann Institute, Dept of
Membrane Research & Biophysics, Rehovot 76100, ISRAEL

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AUTHORS	Kim, P. K. M., Dutra, A., Chandrasekharappa, S. C. and Puck, J. M.
TITLE	Genomic structure and mapping of human FADD, an intracellular mediator of lymphocyte apoptosis
JOURNAL	J. Immunol. (1996) In press
REFERENCE	2 (bases 1 to 1642)
AUTHORS	Kim, P. K. and Puck, J. M.
TITLE	Direct Submission
JOURNAL	Submitted (13-OCT-1996) LGT, NCHGR, NIH, RM 3B07 Bldg. 49, 49

Query Match	78.0%; Score 1326.4; DB 9; Length 1642;
Best Local Similarity	99.9%; Pred. No. 7.1e-214;
Matches 1338; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	
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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:36:05 ; Search time 24.74 Seconds

(without alignments)

400.655 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	108	8.3	521	1 ICEA_HUMAN	Q92851 homo sapien
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36	86	6.6	587	1 YCAO_HAEIN	P44144 haemophilus
37	86	6.6	1453	1 Y373_BOVIN	Q9TU23 bos taurus
38	85.5	6.6	880	1 RA50_PVRAB	Q9U2C8 pyrococcus
39	85	6.5	899	1 PLC1_SCHPO	P40977 schizosacch
40	84.5	6.5	892	1 AAC1_RAT	Q9ZIP2 rattus norv
41	84.5	6.5	903	1 YB56_METJA	O58556 methanococc
42	84	6.5	209	1 TRIC_HUMAN	P19429 homo sapien
43	84	6.5	1957	1 YD86_SCHPO	Q10411 schizosacch
44	83.5	6.4	171	1 CFLA_HSV2	O66674 equine herp
45	83.5	6.4	283	1 LECH_MOUSE	P34927 mus musculu

ALIGNMENTS

RESULT 1
FADD_HUMAN
ID FADD_HUMAN STANDARD; PRT; 208 AA.
AC Q13158; Q14866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FADD protein (FAS-associating death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN FADD OR MOR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS
RC TISSUE-Umbilical vein endothelial cells;
RX MEDLINE=95277837; PubMed=7538907;
RA Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
RT "FADD, a novel death domain-containing protein, interacts with the
RT death domain of Fas and initiates apoptosis.";
RL Cell 81:505-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9529578; PubMed=7536190;
RA Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
RA Wallach D.;
RT "A novel protein that interacts with the death domain of Fas/AP01
RT contains a sequence motif related to the death domain.";
RL J. Biol. Chem. 270:7795-7798(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Lung;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP STRUCTURE BY NMR OF 1-83.
RX MEDLINE=98241233; PubMed=9582077;
RA Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
RA Lenardo M.J., Fesik S.W.;
RT "NMR structure and mutagenesis of the FADD (Mort1) death-effector
RT domain.";
RL Nature 392:941-945(1998).
CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS.
CC -1- SUBUNIT: INTERACTS WITH CFLAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT
CC FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:30:20 ; Search time 16.21 Seconds
(without alignments)
385.747 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VNOAPECRFGGILGPLGKR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1302	100.0	256	5	PCT-US95-16542-2
2	1302	100.0	256	5	PCT-US96-10521-2
3	1047	80.4	208	1	US-08-618-164-3
4	1040	79.9	208	4	US-09-074-044A-19
5	1033	79.3	208	4	US-09-382-155-19
6	1028	79.0	208	4	US-09-064-414-6
7	985.5	75.7	201	4	US-09-064-414-4
8	982.5	75.5	201	4	US-09-064-414-2
9	438	33.6	85	4	US-09-042-785A-28
10	405	31.1	84	1	US-08-665-220-64
11	405	31.1	84	4	US-09-291-692-64
12	401	30.8	83	4	US-09-382-155-15
13	401	30.8	83	4	US-09-074-044A-15
14	382	29.3	74	4	US-08-995-159-5
15	318	24.4	62	4	US-08-894-626-5
16	128.5	9.9	250	4	US-09-187-789-48
17	122	9.4	180	4	US-09-382-155-18
18	122	9.4	180	4	US-09-382-155-18
19	122	9.4	220	2	US-08-807-200-2
20	122	9.4	220	4	US-09-001-777-2
21	122	9.4	235	5	PCT-US96-10521-5
22	122	9.4	257	1	US-08-618-164-2
23	122	9.4	261	5	PCT-US96-10521-25
24	122	9.4	277	5	PCT-US96-10521-8
25	122	9.4	464	5	PCT-US96-10521-18
26	122	9.4	479	2	US-08-807-200-12
27	122	9.4	479	3	US-08-852-782-3

28	122	9.4	479	4	US-09-001-777-12	Sequence 12, Appl
29	122	9.4	479	5	PCT-US96-10521-7	Sequence 7, Appl
30	119	9.1	709	1	US-08-444-005-17	Sequence 17, Appl
31	117	9.0	75	4	US-09-291-692-66	Sequence 66, Appl
32	117	9.0	479	4	US-09-382-155-27	Sequence 27, Appl
33	117	9.0	479	4	US-09-382-155-28	Sequence 28, Appl
34	117	9.0	479	4	US-09-074-044A-27	Sequence 27, Appl
35	117	9.0	479	4	US-09-074-044A-28	Sequence 28, Appl
36	116	8.9	75	1	US-08-665-220-66	Sequence 66, Appl
37	116	8.9	81	2	US-08-807-200-4	Sequence 4, Appl
38	116	8.9	81	4	US-09-001-777-4	Sequence 4, Appl
39	116	8.9	83	4	US-09-382-155-11	Sequence 11, Appl
40	116	8.9	83	4	US-09-074-044A-11	Sequence 11, Appl
41	116	8.9	496	1	US-08-665-220-4	Sequence 4, Appl
42	116	8.9	496	1	US-09-291-692-4	Sequence 4, Appl
43	115.5	8.9	656	1	US-08-444-005-15	Sequence 15, Appl
44	115.5	8.9	656	1	US-09-069-023-28	Sequence 28, Appl
45	114	8.8	479	4	US-09-382-155-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
PCT-US95-16542-2
; Sequence 2, Application PC/TUS9516542
; GENERAL INFORMATION:
; APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
; APPLICANT: WEINMURZEL, Henry
; APPLICANT: WALLACH, David
; APPLICANT: BOLDIN, Mark
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: METT, Igor
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16542
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: IL 112022
; FILING DATE: 15-DEC-1994
; APPLICATION NUMBER: IL 112692
; FILING DATE: 19-FEB-1995
; PRIOR APPLICATION DATA:
; FILING DATE: IL 114615
; APPLICATION NUMBER: 16-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16542-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECFGGGILGPKRRDLARASEPTEGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
Db 1 VNOAPECFGGGILGPKRRDLARASEPTEGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
QY 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
Db 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
Db 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
QY 181 YPRNLTERVRESLRWKNTKENATVAHLVGLALRSQMNVLVADLVQEQVQARDLQNRSGA 240
Db 181 YPRNLTERVRESLRWKNTKENATVAHLVGLALRSQMNVLVADLVQEQVQARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
Db 241 MSPMSWNSDASTSEAS 256

RESULT 2
PCT-US96-10521-2
; Sequence 2, Application PC/TUS9610521
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Braxton, Scott Michael
; TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,164
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0058 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 791038
US-09-824-134-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-132;

Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNOAPECFGGGILGPKRRDLARASEPTEGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
Db 1 VNOAPECFGGGILGPKRRDLARASEPTEGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
QY 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
Db 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
Db 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
QY 181 YPRNLTERVRESLRWKNTKENATVAHLVGLALRSQMNVLVADLVQEQVQARDLQNRSGA 240
Db 181 YPRNLTERVRESLRWKNTKENATVAHLVGLALRSQMNVLVADLVQEQVQARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
Db 241 MSPMSWNSDASTSEAS 256

RESULT 3
US-08-618-164-3
; Sequence 3, Application US/08618164
; Patent No. 5712115
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Braxton, Scott Michael
; TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,164
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0058 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 791038
US-08-618-164-3

Query Match 80.4%; Score 1047; DB 1; Length 208;

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Best Local Similarity 100.0%; Pred. No. 9.9e-105;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 MDPELVLLHSVSSLSSELTELFCLGRVVKRLERVOSGLDLFSMLLEQNDLEPGHT 108
Db 1 MDPELVLLHSVSSLSSELTELFCLGRVVKRLERVOSGLDLFSMLLEQNDLEPGHT 60

Qy 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGVKDWRRLAROLK 168
Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGVKDWRRLAROLK 120

Qy 169 VSDTKIDSIEDRYPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLVADLVQEV 228
Db 121 VSDTKIDSIEDRYPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLVADLVQEV 180

Qy 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
Db 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 4
US-09-074-044A-19
; Sequence 19, Application US/09074044A
; Patent No. 6207458
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,044A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 26588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-074-044A-19

Query Match 79.9%; Score 1040; DB 4; Length 208;
Best Local Similarity 99.5%; Pred. No. 5.6e-104;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 MDPELVLLHSVSSLSSELTELFCLGRVVKRLERVOSGLDLFSMLLEQNDLEPGHT 108
Db 1 MDPELVLLHSVSSLSSELTELFCLGRVVKRLERVOSGLDLFSMLLEQNDLEPGHT 60
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Qy 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGVKDWRRLAROLK 168
Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGVKDWRRLAROLK 120

Qy 169 VSDTKIDSIEDRYPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLVADLVQEV 228
Db 121 VSDTKIDSIEDRYPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLVADLVQEV 180

Qy 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
Db 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 5
US-09-382-155-19
; Sequence 19, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-19

Query Match 79.3%; Score 1033; DB 4; Length 208;
Best Local Similarity 99.0%; Pred. No. 3.2e-103;
Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 49 MDPELVLLHSVSSLSSELTELFCLGRVVKRLERVOSGLDLFSMLLEQNDLEPGHT 108
Db 1 MDPELVLLHSVSSLSSELTELFCLGRVVKRLERVOSGLDLFSMLLEQNDLEPGHT 60

Qy 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGVKDWRRLAROLK 168
Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGVKDWRRLAROLK 120

Qy 169 VSDTKIDSIEDRYPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLVADLVQEV 228
Db 121 VSDTKIDSIEDRYPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLVADLVQEV 180

Qy 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
Db 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 6
US-09-064-414-6
; Sequence 6, Application US/09064414
; Patent No. 6248875
; GENERAL INFORMATION:
; APPLICANT: Wood, Andrew T
; APPLICANT: Bingham, Brendan W
; APPLICANT: Young, Kathleen H
; APPLICANT: Birsan, Camella
; TITLE OF INVENTION: Neuronal Mortl Isoforms
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Andrea C. Walsh
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
```

COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-6

Query Match 79.0%; Score 1028; DB 4; Length 208;
Best Local Similarity 98.6%; Pred. No. 1.1e-102;
Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 49 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
Db 1 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 168
Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 120
QY 169 VSDTKIDSIDRYPNLTERVRESLRWKTEKENATVAHLVGALRSCQNNLVADLVQEV 228
Db 121 VSDTKIDSIDRYPNLTERVRESLRWKTEKENATVAHLVGALRSCQNNLVADLVQEV 180
QY 229 QOARDLQNRSCAMSPMSWNSDASTSEAS 256
Db 181 QOARDLQNRSCAMSPMSWNSDASTSEAS 208

RESULT 7
US-09-064-414-4
Sequence 4, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia
TITLE OF INVENTION: Neuronal Mortl Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-4

Query Match 75.7%; Score 985.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 3.9e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 49 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
Db 1 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 168
Db 58 ----ELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 113
QY 169 VSDTKIDSIDRYPNLTERVRESLRWKTEKENATVAHLVGALRSCQNNLVADLVQEV 228
Db 114 VSDTKIDSIDRYPNLTERVRESLRWKTEKENATVAHLVGALRSCQNNLVADLVQEV 173
QY 229 QOARDLQNRSCAMSPMSWNSDASTSEAS 256
Db 174 QOARDLQNRSCAMSPMSWNSDASTSEAS 201

RESULT 8
US-09-064-414-2
Sequence 2, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia
TITLE OF INVENTION: Neuronal Mortl Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 201 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-064-414-2

Query Match 75.5%; Score 982.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 8.1e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 49 MDPFLVLLHSVSSSSLSSELTEKFLICGRVVKRLERVQSGDLFLSMLEQNDEPGHT 108
Db 1 MDPFLVLLHSVSSSSLSSELTEKFLICGRVVKRLERVQSGDLFLSMLEQNDEPGHT 57
QY 109 ELLRELLASLRHDLRRYDDFEAGAAAGAPCEEDLCAAFNVICDNGKDWRRRLARQLK 168
Db 58 ----ELLASLRHDLRRYDDFEAGAAAGAPCEEDLCAAFNVICDNGKDWRRRLARQLK 113
QY 169 VSDTKIDSTEDRYPRNLTERVRESLRINKTEKENATVAHLVGALRSCQMNVLVADLVOEV 228
Db 114 VSDTKIDSTEDRYPRNLTERVRESLRINKTEKENATVAHLVGALRSCQMNVLVADLVOEV 173
QY 229 QOARDLQNRSGAMPMSWNSDASTSEAS 256
Db 174 QOARDLQNRSGAMPMSWNSDASTSEAS 201

RESULT 9
US-09-042-785A-28
; Sequence 28, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 85 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-28

Query Match 33.6%; Score 438; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.7e-40;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 LCAAFNVICDNGKDWRRRLARQLKVSVDTKIDSTEDRYPRNLTERVRESLRINKTEKENA 204
Db 1 LCAAFNVICDNGKDWRRRLARQLKVSVDTKIDSTEDRYPRNLTERVRESLRINKTEKENA 60
QY 205 TVAHLVGALRSCQMNVLVADLVOEVQ 229
Db 61 TVAHLVGALRSCQMNVLVADLVOEVQ 85

RESULT 10
US-08-665-220-64
; Sequence 64, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note= "human FADD"
US-08-665-220-64

Query Match 31.1%; Score 405; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2.7e-36;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 49 MDPFLVLLHSVSSSSLSSELTEKFLICGRVVKRLERVQSGDLFLSMLEQNDEPGHT 108
Db 1 MDPFLVLLHSVSSSSLSSELTEKFLICGRVVKRLERVQSGDLFLSMLEQNDEPGHT 60

US-09-074-044A-15

Query Match 30.8%; Score 401; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 7.1e-36;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTEKFCIGRVVKRKLERSVQSGLDLFSMLLEQNDLEPGHT 108
|||||
Db 1 MDPFLVLLHSVSSLSSELTEKFCIGRVVKRKLERSVQSGLDLFSMLLEQNDLEPGHT 60
|||||

QY 109 ELLRELLASLRHDLRRVDDFE 131
|||||
Db 61 ELLRELLASLRHDLRRVDDFE 83
|||||

RESULT 14
US-08-995-159-5
; Sequence 5, Application US/08995159
; Patent No. 6130079
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995.159
FILING DATE: Herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,868
FILING DATE: 20-DEC-1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.0860001
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-995-159-5

Query Match 29.3%; Score 382; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.6e-34;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGKDWRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVG 211
|||||
Db 1 ICDNVGKDWRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVG 60
|||||

QY 212 ALRSCQNNLVADLV 225
|||||
Db 61 ALRSCQNNLVADLV 74
|||||

RESULT 15
US-08-894-626-5
; Sequence 5, Application US/08894626
; Patent No. 6355780
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; BOLDIN, Mark P.
; VARFOLOMEEV, Eugene E.
; PANCER, Zeev
; METT, Igor
; GONCHAROV, Tanya M.
; WEINMURZEL, Henry

TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894.626
FILING DATE: 09-Dec-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-894-626-5

Query Match 24.4%; Score 318; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9e-27;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 WRRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVGALRSCQNN 219
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Db 1 WRRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVGALRSCQNN 60
|||||

QY 220 LV 221
||
Db 61 LV 62
||

Search completed: August 17, 2002, 00:37:45
Job time: 445 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2002, 00:34:15 ; Search time 69.07 seconds
(without alignments)
641.186 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VQAPFCRGGGILGPKR.....RSGAMSPWNSDASTSPAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_bacteriophage:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131.5	10.1	482	11 Q9JHX4	Q9JHX4 rattus norv
2	128.5	9.9	476	13 Q918J3	Q918J3 brachydanio
3	125.5	9.6	480	11 Q89110	Q89110 m caspase 8
4	123.5	9.4	239	5 Q9V3B4	Q9V3B4 drosophila
5	122	9.4	276	4 Q96722	Q96722 homo sapien
6	121.5	9.3	1856	4 Q99407	Q99407 homo sapien
7	118.5	9.1	1719	4 Q13768	Q13768 homo sapien
8	118	9.1	941	11 Q61328	Q61328 rattus norv
9	117.5	9.0	1848	11 Q61302	Q61302 mus musculu
10	116.5	8.9	1975	5 Q9VCD1	Q9VCD1 drosophila
11	116	8.9	496	4 Q9COK4	Q9COK4 homo sapien
12	111	8.5	482	13 Q9OWU1	Q9OWU1 gallus gall
13	110	8.4	462	4 Q96TE4	Q96TE4 homo sapien
14	109	8.4	520	13 Q91B62	Q91B62 xenopus lae
15	103.5	7.9	461	5 Q96407	Q96407 lltomosoida
16	103.5	7.9	970	5 Q17342	Q17342 caenorhabdi

17	103.5	7.9	985	5 Q17341	Q17341 caenorhabdi
18	103.5	7.9	1786	5 Q17344	Q17344 caenorhabdi
19	103	7.9	1809	5 Q17487	Q17487 caenorhabdi
20	103	7.9	1815	5 Q17488	Q17488 caenorhabdi
21	103	7.9	1867	5 Q17486	Q17486 caenorhabdi
22	103	7.9	2039	5 Q17489	Q17489 caenorhabdi
23	103	7.9	6994	5 Q17343	Q17343 caenorhabdi
24	101.5	7.8	500	13 Q91B64	Q91B64 xenopus lae
25	100	7.7	2091	5 Q9VJ69	Q9VJ69 drosophila
26	99.5	7.6	218	11 Q99M25	Q99M25 rattus norv
27	99	7.6	919	16 Q9HZA6	Q9HZA6 pseudomonas
28	99	7.6	927	2 Q87015	Q87015 pseudomonas
29	99	7.6	1955	5 Q61308	Q61308 parascaris
30	98	7.5	381	11 Q9Q2M4	Q9Q2M4 mus musculu
31	98	7.5	472	10 Q943N5	Q943N5 oryza sativ
32	97	7.5	487	5 Q9GNM2	Q9GNM2 styela clav
33	97	7.5	622	17 Q9HQ32	Q9HQ32 halobacteri
34	97	7.5	665	4 Q96M89	Q96M89 homo sapien
35	96.5	7.4	1162	10 Q9LY65	Q9LY65 arabidopsis
36	96	7.4	647	16 Q9HUB1	Q9HUB1 pseudomonas
37	95.5	7.3	509	16 Q9A2N4	Q9A2N4 caulobacter
38	95.5	7.3	751	5 Q9NK92	Q9NK92 drosophila
39	95	7.3	406	16 P95251	P95251 mycobacteri
40	95	7.3	414	2 Q9XAF3	Q9XAF3 streptomyce
41	94.5	7.3	333	4 Q9NF94	Q9NF94 homo sapien
42	94.5	7.3	357	13 Q9DF34	Q9DF34 brachydanio
43	94	7.2	222	10 Q9SELS	Q9SELS arabidopsis
44	94	7.2	977	4 Q75300	Q75300 homo sapien
45	94	7.2	977	4 Q9H476	Q9H476 homo sapien

ALIGNMENTS

RESULT 1

Q9JHX4 ID Q9JHX4 PRELIMINARY; PRT; 482 AA.

AC Q9JHX4

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE CASPASE-8.

GN CASP8.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;

RA Cao G., Graham S.H., Chen D., Chen J.;

RT "Molecular cloning and characterization of rat caspase-8: Its

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF279308; AAF87778.1; -

DR EMBL; AF289372; AAK83055.1; -

DR HSSP; Q15806; 10DU;

DR MEROPS; C14.009; -

DR InterPro; IPR003576; Caspase.

DR InterPro; IPR001875; DED.

DR InterPro; IPR002138; ICE_P10.

DR InterPro; IPR001309; ICE_P20.

DR InterPro; IPR002396; IL1Bconv_enz.

DR Pfam; PF01335; DED; 2.

DR Pfam; PF00655; ICE_P10; 1.

DR Pfam; PF00656; ICE_P20; 1.

DR PRINTS; PR00376; IL1BCENZME.

DR SMART; SM00115; CASc; 1.

DR SMART; SM00031; DED; 2.
DR PROSITE; P50112; CASPASE_CYS; 1.
DR PROSITE; P50121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; P50207; CASPASE_210; 1.
DR PROSITE; P50208; CASPASE_210; 1.
DR PROSITE; P50168; DED; 2.
SQ SEQUENCE 482 AA; 55370.00;

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Query Match      10.1%; Score 131.5; DB 11; Length 482;
Best Local Similarity 40.5%; Pred. No. 0.0062;
Matches 32; Conservative 13; Mismatches 34; Indels 1; Gaps 1;

QY 49 MDPFVLVLHVSSTSSLSSELTELKFLGRVVRKLRVQSGLDLFSLMELEONDLEPGHT 108
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Db 1 MD-FHSCLYDIAERLGNELAAKFLCLDHPKKQESINDVLVFLRQLQEEGMLEEDNL 59
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QY 109 ELLRELLASLRHHLLRRV 127
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Db 60 SFKLFLFHISRDLRLSRV 78
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	RESULT	2		PRT;	476 AA.
	Q9I8J3	ID	PRELIMINARY;		
	Q9I8J3	ID	09I8J3		
	DAC		Q9I8J3;		
	DT		01-OCT-2000	(TREMBLrel. 15, Created)	
	DT		01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
	DE		01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
	E		CASPASE-8.		
	N		CASP8.		
	NN		Brachydanio rerio (Zebrafish) (zebra danlio).		
	S		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	SS		Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
	CC		Cypriniformes; Cyprinidae; Danio.		
	OC		NCBI_TaxID=7955;		
	X		[1]		
	XX		NN		

SEQUENCE FROM N.A.
MEDLINE=20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in zebrafish";
Cell Death Differ. 7:509-510(2000).
EMBL; AF273220; ANF79207.1; -
HSP; Q15806; IODU.
MEROPS; C14.009; -
InterPro; IPR003576; Caspase.
InterPro; IPR001875; DED.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; IPR002398; IL1bconv_enz.
Pfam; PF01335; DED; 2.
Pfam; PF00635; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BENZYM.
SMART; SM00115; CASC; 1.
SMART; SM00031; DED; 2.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
PROSITE; PS0168; DED; 2.
SEQUENCE 476 AA; 54990 MW; FD9DFF4B3C31FB9 CRC64;

Query Match 9.9%; Score 128.5; DB 13; Length 476;
Best Local Similarity 28.1%; Pred. No. 0.011;
Matches 59; Conservative 29; Mismatches 83; Indels 39; Gaps 10;

49 MDPFLVLLHSVSSLSSELTELKFLGRVVKRLERVQSGDLDFSMLEQNDLPGHT 108
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1 MDP-QIFREIDENTSGVDQDKFLCLDFIPKRLESVTDAKLIILRDEQGLB---D 55
 109 ELL-RELLASLRHDLRRVDDFEAGANAGAPGEDCAAFNVICDVGKD---WRLLA 164

Db	56	ELLFPFLLIAGRDLLEILKKSKEEV-----ERNL-----: ::: : ::
QY	165	ROLKVSPTKDIDSIEDRY-----PRNLTRBVRESLRHWKTEKENA-----TVHAHLVG 211
Db	104	--LKISE--DMTEENFRAAKFLDLPRAKLGRSTSFIDALIEKQOORLPNDLDELVR 158
QY	212	ALRSCNNVLADLVQVEVQQRDLNRSGAM 241
Db	159	ILEKCDKQLAVMIERFRNQSHRDQQGGRL 188

RESULT	3	
089110	PRELIMINARY;	PRT; 480 AA.
089110	035669;	
AD	01-NOV-1998 (T-EMBLrel. 08, Created)	
RC	01-NOV-1998 (T-EMBLrel. 18, Last sequence update)	
OT	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)	
DT	CASPASE 8 PRECURSOR (EC 3.4.22.-) (CASPASE-8) (ICE-LIKE APOPTOTIC	
DE	PROTEASE 5) (MORTA-ASSOCIATED CED-3 HOMOLOG) (MACH) (FADD-HOMOLOGOUS	
DE	ICE/CED-3-LIKE PROTEASE) (FADD-LIKE ICE) (FLICE) (APOPTOTIC CYSTEINE	
DE	PROTEASE) (APOPTOTIC PROTEASE MCH-5) (CAP4).	
AN	CASP8 OR CASP-8 OR FLICE.	
AN	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
XX	NCBI_TaxID=10090;	
XX	[1]	
IN	SEQUENCE FROM N.A., AND CHARACTERIZATION.	
PP	STRATN=129/SVJ;	
PC	MEDLINE=98316661; Pubmed=9654089;	
XX	Sakamaki K., Tsukumo S.-I., Yonehara S.;	
A	"Molecular cloning and characterization of mouse caspase-8."	
L	Eur. J. Biochem. 253:399-405(1998)	

[2] SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-99057979; PubMed-9837723;
A van de Craen M., Van Loo G., Declercq W., Schotte P.,
A van der Brande I., Mandruzato S., van der Bruggen P., Fiers W.,
T vandenabele P.;
L "Molecular cloning and identification of murine caspase-8.";
[3] J. Mol. Biol. 284:1017-1026(1998).
P SEQUENCE FROM N.A.
A Strausberg R.;
P Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[4] SEQUENCE OF 57-476 FROM N.A.
Kioschis P., Kischkel F., Poustka A., Krammer P.;
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
TNFR-1 INDUCED CELL DEATH. BINDING TO THE ADAPTER MOLECULE FADD
RECRUITS IT TO EITHER RECEPTOR. THE RESULTING AGGREGATE CALLED THE
DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
LIBERATED FROM THE DISC AND ACTIVATES DOWNSTREAM APOPTOTIC
PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE
(CAP3, CAPS AND CAP6) ARE LIKELY RETAINED IN THE DISC. CLEAVES AND
ACTIVATES CASPASE-1, -2, -3, -6, -7, -8, -11/4 AND -12.
-1- FUNCTION: MAY PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS.
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP).
HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-|-AMC
(BY SIMILARITY)
-1- ENZYME REGULATION: INHIBITED BY Z-VAD-FK, CRMA AND P35.
-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
HIGHEST EXPRESSION IN SPLEEN, THYMUS, LUNG, LIVER AND KIDNEY.
LOWER EXPRESSION IN HEART, BRAIN, TESTIS AND SKELETAL MUSCLE.
-1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST EXPRESSION OCCURS AT
DAY 7.
-1- DOMAIN: CONTAINS TWO DEATH EFFECTOR DOMAINS (ALSO CALLED MORT
MODULES) WHICH ARE INVOLVED IN THE BINDING OF CORRESPONDING

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CC CC -1- PTH: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE DISC
CC CC WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC
CC CC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND CASPASE-10 CAN
CC CC BE INVOLVED IN THESE PROCESSING EVENTS (BY SIMILARITY).
CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
CC CC CASPASE FAMILY.
DR EMBL; AF067841; AAC40132.1; -
DR EMBL; AF067835; AAC40132.1; JOINED.
DR EMBL; AF067836; AAC40132.1; JOINED.
DR EMBL; AF067837; AAC40132.1; JOINED.
DR EMBL; AF067838; AAC40132.1; JOINED.
DR EMBL; AF067839; AAC40132.1; JOINED.
DR EMBL; AF067840; AAC40132.1; JOINED.
DR EMBL; AF067834; AAC40131.1; -
DR EMBL; AJ007749; CAA07677.1; -
DR EMBL; BC006641; CAA04196.1; -
DR EMBL; BC006737; AAH06737.1; -
DR HSP; O15806; 1000.
DR MEROPS; C14.009; -
DR MG; MG1:1261423; Casp8.
DR InterPro: IPR003576; Caspase.
DR InterPro: IPR001875; DED.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00855; ICE_P10; 1.
DR Pfam; PF00856; ICE_P20; 1.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0166; DED; 2.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 218 BY SIMILARITY.
FT CHAIN 219 376 CASPASE-8 SUBUNIT P18 (BY SIMILARITY).
FT PROPEP 377 387 BY SIMILARITY.
FT CHAIN 388 480 CASPASE-8 SUBUNIT P10 (BY SIMILARITY).
FT ACT_SITE 319 319 BY SIMILARITY.
FT ACT_SITE 362 362 BY SIMILARITY.
FT DOMAIN 3 80 DEATH EFFECTOR DOMAIN (BY SIMILARITY).
FT DOMAIN 101 177 DEATH EFFECTOR DOMAIN (BY SIMILARITY).
FT CONFLICT 68 71 HISR -> PHPVG (IN REF. 4).
FT CONFLICT 94 99 DNQIS -> RQCPRL (IN REF. 4).
FT CONFLICT 96 96 A -> V (IN REF. 2).
FT CONFLICT 103 107 VMLFK -> SCSFR (IN REF. 4).
FT CONFLICT 475 475 K -> N (IN REF. 4).
SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5ED4F CRC64;

Query Match 9.6%; Score 125.5; DB 11; Length 480;
Best Local Similarity 39.5%; Pred. No. 0.02;
Matches 30; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy 49 MDPEVLVHVSLSSELTFLKFLGRVVRKRVQSLDLSMLENDLEPGHT 108
Db 1 MD-FQSCLYAIAEELGSEDLAALKFLCLDVPHPKQETIEDAKFLRLREKNLEGNL 59

Qy 109 ELLRELLASLRHRLDL 124
Db 60 SFLKELLFHISRWDLL 75

RESULT 4
Q9V3B4 ID Q9V3B4 PRELIMINARY; PRT; 239 AA.
AC Q9V3B4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG12297 PROTEIN (DEATH DOMAIN-CONTAINING ADAPTOR PROTEIN).

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GN BG4 OR CG12297.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RW MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Garg N.S., Gelbart W.M., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasmann D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX Zhou L., Steller H.;
RW MEDLINE=20469420; PubMed=10934188;
RA Hu S., Yang X.;
RT "dFADD, a Novel Death Domain-containing Adapter Protein for the
RN Drosophila Caspase DREDD.";
RX J. Biol. Chem. 275:30761-30764(2000).
RA EMBL; AE003737; AAF55950.1; -
DR EMBL; AF222005; AAF44325.1; -
DR EMBL; AF295103; AAG22535.1; -
DR FlyBase; FBgn0038928; BG4.
DR InterPro: IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
SQ SEQUENCE 239 AA; 27421 MW; F43CFAA546C3FCD9 CRC64;

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Query Match

9.4%; Score 122.5; DB 5; Length 239;

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Query Match      9.38;  Score 121.5;  DB 4;  Length 1856;
Best Local Similarity 27.28;  Pred. No. 0.26;
Matches 34;  Conservative 28;  Mismatches 56;  Indels 7;  Gaps 2;

QY 137 GAAGCEDLCAAFNVICDNGCKDWRRLARLQKVSDTKIDSTEDRYPNLRTVERESLRW 196
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1370 GSLSGTEAQENKMAVIEHGLGSLWAELARLQFVSVDINIRVENPNLSLQSVALLNLW 1439

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QY 197 KNTKENATVAHLVGLRSCOMNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWNSD 249
DB 1430 VIREGQANMENLYTALQSDRGVNNLESGRQSNLKPDRRHTDRDYSLSPSQNGY 1489
QY 250 ASTSE 254
DB 1490 SSLQD 1494

RESULT 7
Q13768 PRELIMINARY; PRT; 1719 AA.
AC Q13768;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE ALT. ANKYRIN (VARIANT 2.2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=HEMATOPOIETIC;
RX MEDLINE=90158830; PubMed=2137557;
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins.";
RL Nature 344:36-42(1990).
DR EMBL; X16609; CAA3461.1; -.
DR HSP; Q00420; 1AWC.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 23.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1719 AA; 189011 MW; F63465D16D975CBF CRC64;

Query Match 9.1%; Score 118.5; DB 4; Length 1719;
Best Local Similarity 28.0%; Pred. No. 0.42; Indels 7; Gaps 2;
Matches 33; Conservative 26; Mismatches 52;

QY 137 GAARGEEDLCAAFNVICNVGDKRRRLARQLKVSIDTIDSDRYPRNLTRVRESLRW 196
DB 1395 GSLSGTEQAENKMAVISHLSLNAELARELQFVEDINRTRVENPSLLEQSVALLNLW 1454
QY 197 KNTKENATVAHLVGLRSCOMNLVADLVQ-EVQOARDLQ-----NRSGAMSPMSWNSD 247
DB 1455 VIREGQANMENLYTALQSDRGVNNLESGRQSNLKPDRRHTDRDYSLSPSQMN 1512

RESULT 8
Q63128 PRELIMINARY; PRT; 941 AA.
AC Q63128;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE CFG2 PROTEIN.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HIPPOCAMPAL DENTATE GYRUS;
RX MEDLINE=96312537; PubMed=8700863;
RA Nedivi E., Feldust S., Theill L., Hevroni D.;
RT "A set of genes expressed in response to light in the adult cerebral
RT cortex and regulated during development.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2048-2053(1996).
DR EMBL; X95466; CAA64740.1; -.
DR InterPro; IPR002017; Spectrin.
SQ SEQUENCE 941 AA; 109037 MW; EC50B042E2AF4248 CRC64;

Query Match 9.1%; Score 118; DB 11; Length 941;
Best Local Similarity 22.7%; Pred. No. 0.21;
Matches 58; Conservative 47; Mismatches 96; Indels 54; Gaps 11;

QY 11 GGILGPLGKRR----DLARASEPRTEGARRAGOPRPRPLADPAMPDFVLVLSVSSLS-- 65
DB 678 GEILSWLKSRLKHLIDVSSNE-----AKRGDELAELSS-SFKALVALLSEVEKMLSNF 731
QY 66 SELTELKFLCLGRVVKRLERVOGQ----LDLFSMLLEQNDLEPGHTELLRE-----LLAS 117
DB 732 GECVOYK-----EIVKSLGLEMSGSESKDEATILDTENLFEAQOMLLRHQOKTKMIS 786
QY 118 LRRHDLRLRVDFEAGAAAGAEEDLCAAFNVICNVGDKRRRLARQLKVSIDTKIDS 177
DB 787 AKRDLQOQMEQOQGGQAG--PGQEEL-----RKLESTLTGLEQS 825
QY 178 EDRYPRNLTRVRESLRINKTEKENATVAHLV-----GALRSCOMNLVADLVQEVQOAR 232
DB 826 RERQER----RIQVSLRKWERFETNKETVYVYLPQTGSSHERFLSFLSLESLSLE 881
QY 233 DLQNRSGAMSPMSWN 247
DB 882 EFSKRTESIATQAEEN 896

RESULT 9
Q61302 PRELIMINARY; PRT; 1848 AA.
AC Q61302;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ERYTHROID ANKYRIN.
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=NEURAL;
RX MEDLINE=93252825; PubMed=8486643;
RA Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
RA Barker J.E.;
RT "Complex patterns of sequence variation and multiple 5' and 3' ends
RT are found among transcripts of the erythroid ankyrin gene.";
RL J. Biol. Chem. 268:9533-9540(1993).
DR EMBL; X69063; CAA48801.1; -.
DR HSP; Q00420; 1AWC.
DR MGD; MGI:88024; Ank1.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 23.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.

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DR SMART; SM00248; ANK; 22.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS00088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1848 AA; 202577 MW; 5744BECBF9EBA056 CRC64;

Query Match
Best Local Similarity 9.0%; Score 117.5; DB 11; Length 1848;
Matches 31; Conservative 29; Mismatches 44; Indels 7; Gaps 2;

Qy 151 VICNVGKMDRLRLARQLKVDSTKIDSDRYPRNLTRVRESLRINKTEKENATVAHLV 210
Db 1421 VIREHLGLSMAELARELQFSVEDINRINVENPNLSLLDSTALLTLWDREGENAKNELY 1480
Qy 211 GALSRCNNLVADLVQ-EVQOARDLQ-----NRSGMSPMSWNSDASTSE 254
Db 1481 TALNRIDRSEIVNMLEVSGRQSRNLKPRRHGRDREYSLSQVNGYSSLOD 1531

RESULT 10
Q9VCD1 ID Q9VCD1 PRELIMINARY; PRT; 1975 AA.
AC Q9VCD1
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CG6129 PROTEIN.
GN CG6129
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidenkiam I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrlskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003745; AAF56238.1; -.
DR FlyBase; FBgn0039152; CG6129.
DR InterPro; IPR001871; bZIP.
DR SMART; SM00338; BRL2; 1.
SQ SEQUENCE 1975 AA; 224509 MW; 62BA92C10D3478CC CRC64;

Query Match
Best Local Similarity 8.9%; Score 116.5; DB 5; Length 1975;
Matches 66; Conservative 45; Mismatches 105; Indels 65; Gaps 13;

Qy 10 GGGILGPGKRRDLARASEPRTEGARRAGPQPRPLADPAMPDFVLVLSVSSSSSELT 69
Db 479 GGGGKSP---RRNSTRSQAFAECTISA-----VQAALHKYQLALHDMQVKFQNTSET 528
Qy 70 ELKFLCLGRVYKRLERVQSGLDLFSMLLEQ--NDLEPGHTELLRELLASLRHDLRLV 127
Db 529 L-----RTTKAQLTSEGTQKLLTTKMQOLTTEKLDSSNSK-LSELQ---ERESLORGL 578
Qy 128 DFEAGAAAGAPGEDLCAAFNVICDNVKGKDRRLARQLKVDTKIDSIED----- 179
Db 579 DDIRV-QKQSEMGADINSAP----ENLSSDYKMQNLCKLOKRIIDMEEDKAVELE 633
Qy 180 ----RYPRNLTE-----RVRE---SLRIWKN-----TEKENATVAHLV 213
Db 634 IQRILKDKNITELNLRSEEDRSSRLREETISLREELNRYSLNRLLEQORTESNLINLL 693
Qy 214 RSCOMNLVADLVQEVQOARDLQNRSGMSPMSWNSDASTSE 254
Db 694 EKQKSDLEYDLKLLKCKDLQERHEKLS-----NNSCSTSD 730

RESULT 11
Q9COK4 ID Q9COK4 PRELIMINARY; PRT; 496 AA.
AC Q9COK4
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE CASPASE-8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100893; PubMed=11161814;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.,
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: Candidate genes for ALS2.";
RL Genomics 71:200-213(2001).
DR EMBL; AB038985; BAB32555.1; JOINED.
DR EMBL; AB038982; BAB32555.1; JOINED.
DR EMBL; AB038983; BAB32555.1; JOINED.
DR EMBL; AB038984; BAB32555.1; JOINED.
DR HSP; Q15806; IQDU.
DR InterPro; IPR003576; Caspase.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; IL1Bconv_enz.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
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RESULT 13
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AC Q96TE4;
PRELIMINARY; PRT; 462 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
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GN	XCASPASE-10.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20209426; PubMed=10744739;
RA	Nakajima K., Takahashi A., Yaoita Y.;
RT	"Structure, expression and function of the xenopus laevis caspase
RT	family.";
RL	J. Biol. Chem. 275:10484-10491(2000).
DR	EMBL: AB038173; BAA94751.1; "
DR	HSSP: Q15806; IQDU.
DR	MEROPS: C14.UFW. -.
DR	InterPro: IPR003576; Caspase.
DR	InterPro: IPR001875; DED.
DR	InterPro: IPR002138; ICE p10.

DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; ILIbconv_enz.
DR Pfam: PF01335; DED; 2.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILIbCENZYME.
DR SMART: SM00115; CASC; 1.
DR SMART: SM00031; DED; 2.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
DR PROSITE: PS0168; DED; 2.
SQ SEQUENCE 520 AA; 59626 MW; 331645A09CA6615 CRC64;

Query Match 8.4%; Score 109; DB 13; Length 520;
Best Local Similarity 25.6%; Pred. No. 0.54;
Matches 53; Conservative 35; Mismatches 89; Indels 30; Gaps 8;
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DB 1 MD-FNSMLLRIDDDGLGREDIEALKFLCRDVLKRNKLLSVOSGHFLQQLMTEDLINEDNY 59
QY 109 ELRLRELLASLRHDLRRV--DDFEAGAA---GAAPGEEDLCRAFNVICDNV-CKDWR 161
DB 60 FLGELLYIINHSLHLDGTVKVEVKALPHHWKISPYRQMLYE----LSENVGTGEDEK 115
QY 162 RLARQLKVSDTKIDSTEDRYPRNLTERVRESRIWKNTEKENVATVAHLVGLRSCOMNLV 221
DB 116 RLFLFIL-----PLHKHKENKT-----FLDVLQLEKENAITEEDNVKLLVEEVRKVS 162
QY 222 ADLVEVQVQARDLQNR-----SGAMSP 243
DB 163 PDLKTIERYKERGDKLHRPEIGLMQP 189

RESULT 15
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AC O96407;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANKYRIN HOMOLOG (FRAGMENT).
GN E1.
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Domeyer A.N., Gallin M., Ertmann K.D.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039830; AAC98928.1; -
DR InterPro: IPR00488; Death.
DR Pfam: PF00531; Death; 1.
DR SMART: SM00005; DEATH; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
FT NON_TER 1
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Best Local Similarity 35.2%; Pred. No. 1.3;
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DB 154 IGADWHRRLARALEVPDIDIROVRHQF---VGLEATILRIWRFLLKKEQTAPA----ALRS 206
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Db 207 AFQRIGRDDVVREMNRAEKPDDEGTSGTSSIS 237
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: August 17, 2002, 00:37:15 ; Search time 1697.03 seconds
(without alignments)
13528.530 Million cell updates/sec
Title: US-09-824-134-1
Perfect score: 1701
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_plo.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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2	999.2	58.7	1081 9	AL575812	AL575812
3	981	57.7	1034 9	AL528456	AL528456
4	973.6	57.2	1031 9	AL570642	AL570642
5	953.8	56.1	983 9	AL573044	AL573044
6	933.2	54.9	956 9	AL548504	AL548504
7	924	54.3	973 9	AL527771	AL527771
8	885.6	52.1	912 9	AL528496	AL528496
9	872.8	51.3	955 9	AL562839	AL562839
10	862.4	50.7	961 9	AL521788	AL521788
11	846	49.7	854 9	AL527192	AL527192
12	843.6	49.6	1038 9	AL575732	AL575732
13	827	48.6	922 9	AL518571	AL518571
14	826.2	48.6	859 9	AL556073	AL556073
15	812.6	47.8	859 9	AL517525	AL517525
16	810.8	47.7	897 9	AL530789	AL530789
17	784.4	46.1	880 9	AL530790	AL530790

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	19	772	45.4	859	10	BG751059	BG751059
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	21	767	45.1	1084	10	BE794964	BE794964
	22	751.8	44.2	794	9	AL557131	AL557131
	23	740	43.5	856	10	BI258492	BI258492
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	25	723.8	42.6	793	10	BI196859	BI196859
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	27	716.8	42.1	754	10	BE533599	BE533599
	28	711.2	41.8	739	9	AL552532	AL552532
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	30	707.8	41.6	790	10	BG110153	BG110153
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	32	706	41.5	1122	10	BG248260	BG248260
	33	702	41.3	955	10	BG253228	BG253228
	34	701.8	41.3	766	10	BE799691	BE799691
	35	700.6	41.2	762	10	BI160584	BI160584
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	37	690.4	40.6	1035	10	BF982380	BF982380
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	39	672.4	39.5	719	10	BE275002	BE275002
	40	669	39.3	887	10	BG169352	BG169352
	41	667.4	39.2	870	10	BE888978	BE888978
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ALIGNMENTS

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DEFINITION AL544558 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODI0211021 5
prime, mRNA sequence.
ACCESSION AL544558 GI:12877038
VERSION AL544558.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1117)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 228 a 325 c 359 g 196 t 9 others
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VERSION					
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AUTHORS					
TITLE					
JOURNAL					
COMMENT					
Contact: Genoscope					
Genoscope - Centre National de Sequencage					
BP 191 91006 EVRY cedex - France					
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					
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QY	634	GTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCAGCAGGCC	693		
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Db	958	CGTGACCTCCAGAACAGGAGTGGGGCCATGTCTCCCGATGTCTGGAATCAGACGCATCT	899		
QY	754	ACCTCCGAAGCGTCTGTATGGCGCGTGTTCGGCTGGTGGACACAGCATCTACACA	813		
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QY	814	GCCTGGACTTTGGTCTCTCCAGGAAGTACCCAGACCTGTGGAAGACCCAGCAGGAAGC	873		
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VERSION AL528456.1 GI:12791949
KEYWORDS EST.
SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1034)
L1.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 239 a 295 c 269 g 224 t 7 others
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VERSION
AL570642.1 GI:12927150
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1031)
Li W.B., Gruber C., Jesse J., and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 248 a 297 c 268 g 212 t 6 others
ORIGIN

Query Match 57.2%; Score 973.6; Db 9; Length 1031;
Best Local Similarity 98.2%; Pred. No. 9.8e-156;
Matches 1012; Conservative 3; Mismatches 13; Indels 3; Gaps 3;

Qy 616 GTGGCCACCTGGTGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTA 675
Db 1031 STGCCCCACCTGGTGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTA 972

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Qy 676 CAAGAGTTTCAGCAGGCCGCTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 735
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Qy 736 TGGAACTCAGACGATCTACCTCCGAAGCGTCTCTGATGGCCGCTGCTTTGGCGTGGTG 795
Db 912 TGGAACTCAGACGATCTACCTCCGAAGCGTCTCTGATGGCCGCTGCTTTGGCGTGGTG 853
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Db 852 ACCACAGGATCTACACAGCGCTGGACTTTTGTCTCTCCAGGAAGGTAGCCAGCAGTGT 793
Qy 856 GAAGACCCAGCAGGAGGAGGCTGAGTGGCCACAGACACCTGCTTCTGAACCTCAAG 915
Db 792 GAAGACCCAGCAGGAGGAGGCTGAGTGGCCACAGACACCTGCTTCTGAACCTCAAG 733
Qy 916 TGGCTTTTAAATGCTCTCCGACAGCGCGGCTTGGGCCCTGCACAGATATTCCA 975
Db 732 TGGCTTTTAAATGCTCTCCGACAGCGCGGCTTGGGCCCTGCACAGATATTCCA 673
Qy 976 TTTCTTCTCCTCATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCCTCGGGA 1035
Db 672 TTTCTTCTCCTCATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCCTCGGGA 613
Qy 1036 GTAGTTGGAAAGTTGGAACCGTGTCCAGCACAGAGGAATCTGTCCAGATGAGCAGTCA 1095
Db 612 GTAGTTGGAAAGTTGGAACCGTGTCCAGCACAGAGGAATCTGTCCAGATGAGCAGTCA 553
Qy 1096 ACTGTTACTCCAGCGGAGGAGACAGCTCAGAGGCCAGGAATCGGAGCGAAGCAGAG 1155
Db 552 ACTGTTACTCCAGCGGAGGAGACAGCTCAGAGGCCAGGAATCGGAGCGAAGCAGAG 493
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Db 492 AGGTGGAGCACTGGGATTTGAACCCCGCCATCTTACCAGAGCCCATGCTCAACCACT 433
Qy 1216 GTGGGCTTCTGTCGCCCTGCGAGTTGGCAGAAAGATGTTTTGTGCCATTTCTTTGAG 1275
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Qy 1276 GCCACCGGAGACAGCTGACACTAGGCTCAGCGGGGTGCTGTGGTGGGAGAGGAGCAT 1335
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Qy 1336 GCTGGGTGGGGTGGGAGACCTGTTGGCGGTGGTCCAGCTCTTGGCCCTGCTGTGAG 1395
Db 313 GCTGGGTGGGGTGGGAGACCTGTTGGCGGTGGTCCAGCTCTTGGCCCTGCTGTGAG 254
Qy 1396 TTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGGTGGCAGGACGAATTTGAG 1455
Db 253 TTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGGTGGCAGGACGAATTTGAG 194
Qy 1456 ATAATATCTGTAGGTGCTGATGATGATTGACACAGCAGTCTCTAAATCTCCTTGT 1515
Db 193 ATAATATCTGTAGGTGCTGATGATGATTGACACAGCAGTCTCTAAATCTCCTTGT 134
Qy 1516 GAGATATGGGCTCCTCAATTTACAGTTTCTTACTGTTTGTAT-CAAAATCAGTATC 1574
Db 133 GAGATATGGGCTCCTCAATTTACAGTTTCTTACTGTTTGTATGCAAAATCAGTATC 74
Qy 1575 TTTCTGATAACAGAAATGCCAAGGACGCGGATCTCGTATCTTTAAAAGCAGTCTCTT 1634
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Qy 1635 ATTCCTTAAGT 1645
Db 13 TTTCTCTTGT 3

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RESULT 5
AL573044/c
LOCUS
DEFINITION
AL573044 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1014Y005 3

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ACCESSION prime.. mRNA sequence.
VERSION AL573044
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 230 a 277 c 252 g 219 t 5 others
ORIGIN

Query Match 56.1%; Score 953.8; DB 9; Length 983;
Best Local Similarity 99.0%; Pred. No. 2.3e-152;
Matches 975; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

QY 665 CTGACCTGGTACAGAGTTTCAGAGGCCCTGACCTCCAGAACAGAGTGGGCCCATGT 724
DB 983 CTGACCTGGTACAGAGTTTCAGAGGCCCTGACCTCCAGAACAGAGTGGGCCCATGT 924
QY 725 CCCGATGTCATGGAATCAGACGCATCTACCTCCGAAGCGTCTGATGGCCGCTGCTT 784
DB 923 CCCGATGTCATGGAATCAGACGCATCTACCTCCGAAGCGTCTGATGGCCGCTGCTT 864
QY 785 TGGCGTGGTACACAGGCATCTACAGCGCTGGACTTTGGTTCTCTCCAGGAAGGTAG 844
DB 863 TGGCGTGGTACACAGGCATCTACAGCGCTGGACTTTGGTTCTCTCCAGGAAGGTAG 804
QY 845 CCCAGCACTGTGAAGACCCAGCAGGACCGCTGAGTGAGCCACAGACCACTGCTTC 904
DB 803 CCCAGCACTGTGAAGACCCAGCAGGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTC 744
QY 905 TGAACCTCAAGCTGCTTTATTATGCTCTCCGCGACCGCGGCTTGGGCCCTGCGAC 964
DB 743 TGAACCTCAAGCTGCTTTATTATGCTCTCCGCGACCGCGGCTTGGGCCCTGCGAC 684
QY 965 AGATATTTCATTTCTCCACTATGACACTGAGCAAGATCTTGCTCCACTAAATGAG 1024
DB 683 AGATATTTCATTTCTCCACTATGACACTGAGCAAGATCTTGCTCCACTAAATGAG 624
QY 1025 CTCCTCGGGAGTAGTTGGAACCGTGTCCAGCAGAGAGGATCTGTGCGACA 1084
DB 623 CT-CTCGGGAGTAGTTGGAACCGTGTCCAGCAGAGAGGATCTGTGCGACA 565
QY 1085 TGAGCAGTACACTGTATCTCCACAGCGGAGGAGACCACTCAGAGGCCAGGAATCGGA 1144
DB 564 TGAGCAGTACACTGTATCTCCACAGCGGAGGAGACCACTCAGAGGCCAGGAATCGGA 505

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QY 1145 GCGAAGCAGAGAGGTGGAGAACTGGGATTGTAACCCCGCCCATCTTCCACAGAGCCCAT 1204
DB 504 GCGAAGCAGAGAGGTGGAGAACTGGGATTGTAACCCCGCCCATCTTCCACAGAGCCCAT 445
QY 1205 GCTCAACCACTGTGGCGTTCTGCTGCCCTCAGTTGGCAGAAAGGATGTTTTGTGCCA 1264
DB 444 GCTCAACCACTGTGGCGTTCTGCTGCCCTCAGTTGGCAGAAAGGATGTTTTGTGCCA 386
QY 1265 TTTCTCTGGAGGCCACCGGGACACACCTGGACACTAGGGTCAGCGGGGTGCTGTGGTGG 1324
DB 385 TTTCTCTGGAGGCCACCGGGACACACCTGGACACTAGGGTCAGCGGGGTGCTGTGGTGG 326
QY 1325 GGAGAGCATGGTGGGTGGGGTGGGAGACCTGCTGGCGGTGGTGGCGCTGTTGGC 1384
DB 325 GGAGAGCATGGTGGGTGGGGTGGGAGACCTGCTGGCGGTGGTGGCGCTGTTGGC 266
QY 1385 CCCGTGTGAGTTGAGTCTCTCTCTGAGACTGCTAGTAGTAGGGGCGAGTGTGGCCAG 1444
DB 265 CCCGTGTGAGTTGAGTCTCTCTCTGAGACTGCTAGTAGTAGGGGCGAGTGTGGCCAG 206
QY 1445 GACGAATTGAGATAATATCTGTGAGTGTGATGATGATTGACACACAGCACTCTCTAA 1504
DB 205 GACGAATTGAGATAATATCTGTGAGTGTGATGATGATTGACACACAGCACTCTCTAA 146
QY 1505 ATCTTCCTCTGAGGATATGGTCTCTGCAATCTACAGTTCTTACTGTTTGTATCAA 1564
DB 145 ATCTTCCTCTGAGGATATGGTCTCTGCAATCTACAGTTCTTACTGTTTGTATCAA 86
QY 1565 AATCACTATCTTCTGATACAGAAATGCCAGGACGGGATCTCGTATCTTTAAAG 1624
DB 85 AATCACTATCTTCTGATACAGAAATGCCAGGACGGGATCTCGTATCTTTAAAG 26
QY 1625 CAGTCTCTTATTCCTAAGGTAATC 1649
DB 25 CAGTCTCTTATTCCTAAGGTAATC 1

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RESULT 6
LOCUS

AL548504 956 bp mRNA linear EST 16-FEB-2001
AL548504 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI014YM05 5
prime, mRNA sequence.

ACCESSION AL548504

VERSION AL548504.1 GI:12883573

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..956

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/clone="CS0DI014YM05"

/clone_lib="LTI_NFL006_PL2"

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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

BASE COUNT	194 a	288 c	318 g	155 t	1 others
ORIGIN	http://fulllength.invitrogen.com"				

Query Match 54.9%; Score 933.2; DB 9; Length 956;
Best Local Similarity 99.6%; pred. No. 7.1e-149;
Matches 946; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY	1	GTGAATCAGGACCGAGTGCAGGTTCTGGGGGTGGAATCCTTTGGGCCGCTGGGCAACGGG	60
Db	7	GTGAATCAGGACCGAGTGCAGGTTCTGGGGGTGGAATCCTTTGGGCCGCTGGGCAACGGG	66
QY	61	CGAGACCTTGGCCAGGGCCAGCGAGCCGAGACAGAGGGCGCGAGGGCGGGCCGCAG	120
Db	67	CGAGACCTTGGCCAGGGCCAGCGAGCCGAGACAGAGGGCGCGAGGGCGGGCCGCAG	126
QY	121	CCCGGGCCGCTTGCAGACCCCGCCATGTGACCCGTTCCCTGGTGTCTGCTGTGCACCTCGGTGTG	180
Db	127	CGCGGGCGCTTGCAGACCCCGCCATGTGACCCGTTCCCTGGTGTCTGCTGTGCACCTCGGTGTG	186
QY	181	TCCAGCCTGTGAGCAGCGAGCTGACCGAGCTCAAGTTCCCTATGCCCTGGGGCGCGTGGTC	240
Db	187	TCCAGCCTGTGAGCAGCGAGCTGACCGAGCTCAAGTTCCCTATGCCCTGGGGCGGTGGC	246
QY	241	AAGCGCAAGCTGG - AGCGGGTGCAGAGCGGCTAGACCTCTTCCATNGTGTGTGGAGCA	299
Db	247	AAGCGCAAGCTGNGAGGGCGTGCAGAGGGCTAGACCTCTTCCATNGTGTGTGGAGCA	306
QY	300	GAACGACCTGGAGCCCGGGCACACCGAGCTCTCTGGCGGAGTGTCTGCCCTCCCTGGGGG	359
Db	307	GAACGACCTGGAGCCCGGGCACACCGAGCTCTCTGGCGGAGTGTCTGCCCTCCCTGGGGG	366
QY	360	CCAGCAGCTGCTGGCGGGGTGCAGAGCTTCGAGCGGGGGCGCGCGGGGCGCGCC	419
Db	367	CCAGCAGCTGCTGGCGGGGTGCAGAGCTTCGAGCGGGGGCGCGCGGGGCGCGCC	426
QY	420	TGGGAAGAAGACCTGTGTGCAGCATTTAAAGTCTCATATGTGTAATGTGGGGAAGATTG	479
Db	427	TGGGAAGAAGACCTGTGTGCAGCATTTAAAGTCTCATATGTGTAATGTGGGGAAGATTG	486
QY	480	GAGAGGCTGGCTGTCTGAGCTCAAAAGTCTCAGACCAAGATCGACAGCATCGAGGACAG	539
Db	487	GAGAGGCTGGCTGTCTGAGCTCAAAAGTCTCAGACCAAGATCGACAGCATCGAGGACAG	546
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QY	600	GAAGAGAAACGCAACAGTGGCCACCTCGTGGGGGCTCTCAGGCTCGCGAGATGAACCT	659
Db	607	GAAGAGAAACGCAACAGTGGCCACCTCGTGGGGGCTCTCAGGCTCGCGAGATGAACCT	666
QY	660	GTTGGCTGACCTGTTACAAGAGTTTACAGAGGCCGTGACCTCCAGAACAGAGTGGGGC	719
Db	667	GTTGGCTGACCTGTTACAAGAGTTTACAGAGGCCGTGACCTCCAGAACAGAGTGGGGC	726
QY	720	CATGTCCCCGATGTGATGGAAGTCTCAGAGCATCTACCTCGAAGCGTCTCTGATGGGCGC	779
Db	727	CATGTCCCCGATGTGATGGAAGTCTCAGAGCATCTACCTCGAAGCGTCTCTGATGGGCGC	786
QY	780	TGCTTTGGCCTGGTGGACCAACAGCATCTACAGAGCTGAGCTTTGGTCTCTCCAGGAA	839
Db	787	TGCTTTGGCCTGGTGGACCAACAGCATCTACAGAGCTGAGCTTTGGTCTCTCCAGGAA	846
QY	840	GGTAGCCACAGCACTGTGAAGACCCAGAGGACCCAGGCTGAGTGAGCCACAGACCACT	899
Db	847	GGTAGCCACAGCACTGTGAAGACCCAGAGGACCCAGGCTGAGTGAGCCACAGACCACT	906
QY	900	GCTTCTGAATCAAGCTGCGGCTTTTAAATGCCCTCTCCCGCACCAGGCGG	949
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RESULT 7
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LOCUS	AL522777.1	973 bp	linear	EST 13-FEB-2001
DEFINITION	AL522777.1 LTI_NFL003_NBC3	Homo sapiens	cDNA clone	CS0DC026P18.5
ACCESSION	AL522777.1	prime, mRNA sequence.		
VERSION	AL522777.1	GI:12791264		
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 973)

REFERENCE
AUTHORS
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)

COMMENT

Genoscope - Centre National de Sequencage
BP 191 91066 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..973

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 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : lifang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT
ORIGIN

Query Match 54.3%; Score 924; DB 9; Length 973;
 Best Local Similarity 98.8%; Pred. No. 2.6e-147;
 Matches 960; Conservative 2; Mismatches 7; Indels 3; Gaps 3;

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135	AGACCCGCCATGAGACCCGGTTCCTGGTCTGCTGCACATCGGTGCTGCTCCAGCCGTGTCAG	194
121	AGACCCGCCATGAGACCCGGTTCCTGGTCTGCTGCACATCGGTGCTGCTCCAGCCGTGTCAG	180
195	CAGCGAGTGACCGAGGTCATAGTTCTATGCTCGGGCGCGTGTGTAAGCGCAAGCTGG	253
181	CAGCGAGTGACCGAGGTCATAGTTCTATGCTCGGGCGCGTGTGTAAGCGCAAGCTGGN	240
254	AGCGGTGCAGAGGGGCGCTAGACCTCTTCCTCATGCTGTGGAGCAGAAGACCTGGAGC	313
241	AGCGGTGCAGAGGGGCGCTAGACCTCTTCCTCATGCTGTGGAGCAGAAGACCTGGAGC	300
314	CCGGGCACACCGAGCTCCTGCGCGAGCTGTGCGCTCCCTCGGCGCCACGACCTGCTGC	373
301	CCGGGCACACCGAGCTCCTGCGCGAGCTGTGCGCTCCCTCGGCGCCACGACCTGCTGC	360
374	GGCGCTGCAGACTTCGAGGCGGGGCGCGCGCCCGGGCGCGCCCTGGGGAGAAAGACC	433


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QY 859 GACCACGAGGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 918
DB 841 GACCACGAGGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 900
QY 919 GTTATTATATGC 930
DB 901 GTTATTATATGC 912

RESULT 9
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LOCUS AL562839 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC019YA19 3
DEFINITION prime, mRNA sequence.
ACCESSION AL562839
VERSION AL562839.1 GI:12911659
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 226 a 273 c 244 g 198 t 14 others
ORIGIN

Query Match 51.3%; Score 872.8; DB 9; Length 955;
Best Local Similarity 96.4%; Pred. No. 1.3e-138;
Matches 922; Conservative 10; Mismatches 18; Indels 6; Gaps 4;

QY 630 GGGGCTCTCAGGCTCCAGATGACCTGGTGGTGGTACCTGGTACAGAGTTTCAGCA 589
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QY 690 GGCCCGTACCTCCAGAACAGAGTGGGGCCATGCCCGATGTCATGGAACTCAGACGC 749
DB 894 GGCCCGTACCTCCAGAACAGAGTGGGGCCATGCCCGATGTCATGGAACTCAGACGC 836
QY 750 ATCTACCTCCGAGGCTCTGATGGCGCGTGTTCGCTGGTGGACACAGGATCTA 809
DB 835 ATCTACCTCCGAGGCTCTGATGGCGCGTGTTCGCTGGTGGACACAGGATCTA 776
QY 810 CACAGCTGACTTTGGTCTCTCCAGGAGGTAGCCAGACTGTGAAGACCCAGCAGG 869
DB 775 CACAGCTGACTTTGGTCTCTCCAGGAGGTAGCCAGACTGTGAAGACCCAGCAGG 716

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QY 870 AACCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 929
DB 715 AACCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 656
QY 930 CTTCTCCCGCACCAGCGGGCTTGGCCCTGCACAGATATTTCCATTTCTTCCTCACTA 989
DB 655 CTTCTCCCGCACCAGCGGGCTTGGCCCTGCACAGATATTTCCATTTCTTCCTCACTA 596
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QY 1407 CTTGAGACTGCTAAGTAGGGGAGTGTGTGTCAGGAGCAATTCAGATAATATCTGT 1466
DB 176 CTTGAGACTGCTAAGTAGGGGAGTGTGTGTCAGGAGCAATTCAGATAATATCTGT 117
QY 1467 GAGGTGCTGATGAGTGTGACACACAGCACTCTCTAAATCTTCTTGTGAGGATATGG 1526
DB 116 GAGGTGCTGATGAGTGTGACACACAGCACTCTCTAAATCTTCTTGTGAGGATATGG 57
QY 1527 GTCTGCAATTTCTACAGTTCTTACTGTTTGTATCAAAATCACTATCTTCTGAT 1582
DB 56 GTCTGCAATTTCTACAGTTCTTACTGTTTGTATCAAAATCACTATCTTCTGAT 1

RESULT 10
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LOCUS AL521788 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB003YK15 3
DEFINITION prime, mRNA sequence.
ACCESSION AL521788
VERSION AL521788.1 GI:12785281
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. 961
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QY	220	CTATGCTCTGGGCGGCTGGTCAAGCGCAAGTGTAGCGGTGCAGAGCGGCTAGACCTC	279
Db	181	CTATGCTCTGGGCGGCTGGGCAAGCGCAAGCGGTGCAGAGCGGCTAGACCTC	240
QY	280	TTCTCCATGCTGCTGGAGCAGAACGACTGGAGCCGGGACACACCGAGCTCTGCGCGAG	339
Db	241	TTCTCCATGCTGCTGGAGCAGAACGACTGGAGCCGGGACACACCGAGCTCTGCGCGAG	300
QY	340	CTGTCTGGCTCCCTGCGCGGCCACGACCTGCTGCGGCGGTGCAGCACTTCGAGCGGG	399
Db	301	CTGTCTGGCTCCCTGCGGCGCCAGACCTGCTGCGGCGGTGCAGCACTTCGAGCGGG	360
QY	400	GGGCGGCGGGCGGCGGCTTGGGGAAGAACACTGCTGTCAGCACTTTAAGCTCATATGT	459
Db	361	GGGCGGCGGGCGGCGGCTTGGGGAAGAACACTGCTGTCAGCACTTTAAGCTCATATGT	420
QY	460	GATAATGTGGGAAGATTTCGAAAGGCTGGCTGCTGACTCAAAAGTCTCAGACACCAAG	519
Db	421	GATAATGTGGGAAGATTTCGAAAGGCTGGCTGCTGACTCAAAAGTCTCAGACACCAAG	480
QY	520	ATCGACAGCATCGAGGACAGATACCCCGCCAACTTGACAGAGCGTGTGCGGAGTCACTG	579
Db	481	ATCGACAGCATCGAGGACAGATACCCCGCCAACTTGACAGAGCGTGTGCGGAGTCACTG	540
QY	580	AGATCTTGGGAAGAACACAGAAAGGAGAACGCAAGTGGCCCCACCTGTTGGGGGCTCTC	639
Db	541	AGATCTTGGGAAGAACACAGAAAGGAGAACGCAAGTGGCCCCACCTGTTGGGGGCTCTC	600
QY	640	AGTCTCTGCCAGATGAACCTGGTGGCTGACCTGGTGTACAAAGAGTTTCAGCAGGCCGTGAC	699
Db	601	AGTCTCTGCCAGATGAACCTGGTGGCTGACCTGGTGTACAAAGAGTTTCAGCAGGCCGTGAC	660
QY	700	CTCCAGAACAGGAGTGGGGCCATGTCCCGATGTCTGGAAGTTCAGACGCATCTACTCTCC	759
Db	661	CTCCAGAACAGGAGTGGGGCCATGTCCCGATGTCTGGAAGTTCAGACGCATCTACTCTCC	720
QY	760	GAAGCGTCTGTATGGGCGGCTGCTTTGGGCTGGTGGACACAGGCATCTACAGCGCTGG	819
Db	721	GAAGCGTCTGTATGGGCGGCTGCTTTGGGCTGGTGGACACAGGCATCTACAGCGCTGG	780
QY	820	ACTTTGGTTCTCTCAGGAAGGTAGCCAGGACACTGTGAAGACCCAGGAGCCAGGCT	879
Db	781	ACTTTGGTTCTCTCAGGAAGGTAGCCAGGACACTGTGAAGACCCAGGAGCCAGGCT	840
QY	880	GAGTAGGCCACAGA	893
Db	841	GAGTAGGCCACARA	854

RESULT 12
 AL575732
 LOCUS
 DEFINITION
 AL575732 LTI_NFL006_P12 Homo sapiens cDNA clone CS0DI070VG22 5 prime, mRNA sequence.
 ACCESSION
 AL575732
 VERSION
 AL575732.1 GI:12937184
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1. (bases 1 to 1038)
 AUTHORS
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE
 Full-length cDNA libraries and normalization
 JOURNAL
 Unpublished (2001)
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: segraf@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. .1038
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 /clone="CSODI070YG22"
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 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>
 207 a 311 c 353 g 165 t 2 others
 BASE COUNT
 ORIGIN

Query Match	49.6%	Score 843.6	DB 9	Length 1038
Best Local Similarity	99.4%	Pred. No. 11e-133		
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Db				
154	GTGAATCAGGCACGGAGTCGAGGTTCTGGGGGTGGAAATCTTGGCCGCTGGGCAACGG 213			
QY 61	CGAGACCTGGCCAGGGCCAGCAGCGAGGACAGACAGAGGGCGCGGAGGGCGGCGCCGAC 120			
Db				
214	CGAGACCTGGCCAGGGCCAGCAGCGAGGACAGGACAGAGGGCGCGGAGGGCGGCGCCGAC 273			
QY 121	CCCGGGCCGTTGACAGCCCGCCATGGACCCCTTCTTGTGTGCTGTGCTGCTGCTGCTGCTG 180			
Db				
274	CCCGGGCCGTTGACAGCCCGCCATGGACCCCTTCTTGTGTGCTGTGCTGCTGCTGCTGCTG 333			
QY 181	TCAGAGCTGTGAGAGCAGAGCTGACCGAGCTCAAGTTCTTATGCTTCGAGCTCGGGCGCGTGGTC 240			
Db				
334	TCAGAGCTGTGAGAGCAGAGCTGACCGAGCTCAAGTTCTTATGCTTCGAGCTCGGGCGCGTGGTC 393			
QY 241	AGCGCAAGCTGGAGCGCTGTCAGAGCGGCCCTAGACCTCTTCTCCATGCTGTGGAGCAG 300			
Db				
394	AAGCGCAAGCTGGAGCGCGTGCAGAGCGCCCTAGACCTCTTCTCCATGCTGTGGAGCAG 453			
QY 301	AACGACCTGGAGCCGGGGCACACCGAGCTCTTGGCGGAGCTGCTGCCTTCCCTGGGGCGC 360			
Db				
454	AACGACCTGGAGCCGGGGCACACCGAGCTCTTGGCGGAGCTGCTGCCTTCCCTGGGGCGC 513			
QY 361	CACGACCTGCTCGCGCGGCTCGACACTTCGAGGGGGGGCGGCGCGCGCGCGCGCT 420			
Db				
514	CACGACCTGCTCGCGCGGCTCGACACTTCGAGGGGGGGCGGCGCGCGCGCGCGCT 573			
QY 421	GGGGAAGAGACCTGTGTGCAGCATTTAACGTCATATGTGATAATGTGGGAAGATTGG 480			
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574	GGGGAAGAGACCTGTGTGCAGCATTTAACGTCATATGTGATAATGTGGGAAGATTGG 633			
QY 481	AGAGGCTGGCTGCTGTCAGCTCAAAAGTCTCAGACACCAAGATCGACAGCATCGAGACAGA 540			
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634	AGAGGCTGGCTGCTGACCTCAAAAGTCTCAGACACCAAGATCGACAGCATCGAGACAGA 693			
QY 541	TACCCCGCAACCTCGACAGACGGTGTGGGGAGTCACTGAGAATCTGGAAGAACACAGAG 600			
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694	TA-CCCCGCAACCTGACAGACGGTGTGGGGAGTCACTGAGAATCTGGAAGAACACAGAG 752			
QY 601	AAGGAGAACGCAACAGTGGCCCCACTGGTGGGGGCTCTCAGGTCCTGCCAGATGAACCTG 660			
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753	AAGGAGAACGCAACAGTGGCCCCACTGGTGGGGGCTCTCAGGTCCTGCCAGATGAACCTG 812			
QY 661	GTGGCTGACCTGGTACAAAGAGGTTACAGAGCCCGCTGACCTCCAGAACAGAGATGGGGCC 720			
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813	GTGGCTGACCTGGTACAAAGAGGTTACAGAGCCCGCTGACCTCCAGAACAGAGATGGGGCC 872			

QY 721 ATGTCCCGCATGTCTATGAACTCAGACGCTACCTCCGAAGCGTCTCTGATGGCGGCT 780
 Db 873 ATGTCCCGCATGTCTATGAACTCAGACGCTACCTCCGAAGCGTCTCTGATGGCGGCT 932
 QY 781 GCTTTGGCTGGTGGACCAAGGATCTACAGGCTGGAGCTTGTCTCTCCAGGAAG 840
 Db 933 GCTTTGGCTGGTGGACCAAGGATCTACAGGCTGGAGCTTGTCTCTCCAGGAAG 992
 QY 841 GTAGCCAGCACTGTGAAGACC 862
 Db 993 GTAGCCAGCACTGTGAAGACC 1014

RESULT 13
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 LOCUS AL518571 LTI_NFL011_NBC1 932 bp mRNA linear EST 13-FEB-2001
 DEFINITION prime, mRNA sequence.
 ACCESSION AL518571
 VERSION AL518571
 KEYWORDS EST.
 SOURCE AL518571.1 GI:12782064
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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BASE COUNT 189 a 273 c 311 g 154 t 5 others
 ORIGIN

Query Match 48.6%; Score 827; DB 9; Length 932;
 Best Local Similarity 97.3%; Pred. No. 7.6e-131;
 Matches 890; Conservative 4; Mismatches 14; Indels 7; Gaps 5;

QY 1 GTGAATCAGGACCGGAGTGGAGTTCGGGGGTGGAATCTTGGCCCTGGGCAAGCGG 60
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 Db 84 CGAGACCTGGCCAGGCGGAGGACGAGGCGCGGAGGCGGCGGCGGCGGCGGCGG 143
 QY 121 CCGGCGGCGGCTGACAGCCCGGCGGATGACCCGCTTCTGCTGCTGCTGCTGCTG 180
 Db 144 CCGGCGGCGGCTGACAGCCCGGCGGATGACCCGCTTCTGCTGCTGCTGCTGCTG 203

QY 181 TCAGGCTCTGAGGAGGAGGAGTACCGAGCTCAAGTTCTCTATGCTGGGCGCGTGGTC 240
 Db 204 TCAGGCTCTGAGGAGGAGGAGTACCGAGCTCAAGTTCTCTATGCTGGGCGCGTGGTC 263
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 Db 264 AAGCCCAAGCTGGNAGCGGCTGACAGGCGGCTAGACCTCTTCTCCATGCTGCTGGAGCA 323
 QY 300 GAACGACCTGGAGCCCGGCGCACACGAGCTCTGCGCGAGCTGCTGCGCTCCCTGCGGCG 359
 Db 324 GAACGACCTGGAGCCCGGCGCACACGAGCTCTGCGCGCA-CTGCTGCGCTCCCTGCGGCG 382
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 QY 420 TGGGGAAGAAGACCTGCTGCGAGCAATTTAAGCTCATATGTATATGTGGGGAAGATTG 479
 Db 443 TGGGGAAGAAGACCTGCTGCGAGCAATTTAAGCTCATATGTATATGTGGGGAAGATTG 502
 QY 480 GAGAAGGCTGCTGCTGAGCTCAAGTCTCAGACACCAAGATCGACAGCATCGAGGACAG 539
 Db 503 GAGAAGGCTGCTGCTGAGCTCAAGTCTCAGACACCAAGATCGACAGCATCGAGGACAG 562
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 Db 563 ATACCCCGCAACCTGACAGAGCGTGTGCGGAGTCACTGAGATCTGGAAGAACAAGCA 622
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 Db 623 GAAGGAGAACCAACAGTGGCCACCTGGTGGGGGCTCTCAGGTCCTGCCAGATGAACCT 682
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 Db 863 GGTAG-CCAGCACTGTGAAAGCC--AGCAGGAGCCAGGCTGAGTGGAGCC--AAAGACCACT 917
 QY 900 GCTTCTGAATCAAG 914
 Db 918 GCTTCTGAATCAAS 932

RESULT 14
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 LOCUS AL556073 LTI_NFL006_PL2 859 bp mRNA linear EST 16-FEB-2001
 DEFINITION prime, mRNA sequence.
 ACCESSION AL556073
 VERSION AL556073.1 GI:12898410
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
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 /clone="CS0DA003YJ07"
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 /note="Vector: pCMVSPORT 6; Site1: NotI; 1st strand cDNA enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 175 a 253 c 288 g 133 t 10 others
 ORIGIN

Query Match 48.6%; Score 826.2; DB 9; Length 859;
 Best Local Similarity 98.3%; Pred. No. 1e-130;
 Matches 844; Conservative 10; Mismatches 3; Indels 2; Gaps 2;

QY 26 TCGGGGTGGAATCCTTGGCGCGCTGGCAAGCGCGGAGACCTGCCAGGGCCAGCGAGC 85
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 QY 86 CGAGGACAGAGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 145
 Db 61 CGAGGACAGAGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 120
 QY 146 TCGACCCGTTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205
 Db 121 TCGACCCGTTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 206 CCGAGCTCAAGTTCCTATGCTCGCGCGCGCTGGTCAAGCGCAAGCTGG -ACGCGGTGCG 264
 Db 181 CCGAGCTCAAGTTCCTATGCTCGCGCGCGCTGGTCAAGCGCAAGCTGG -AAGCGGTGCG 240
 QY 265 ACGGCGCTAGACCTCTTCATGCTGCTGAGCAGACGACCTGGAGCGCGCGCGCACACC 324
 Db 241 ACGGCGCTAGACCTCTTCATGCTGCTGAGCAGACGACCTGGAGCGCGCGCGCACACC 300
 QY 325 GAGCTCCTCGCGGAGCTGCTCGCTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 384
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 Db 361 GACTTCGAGCG 420
 QY 445 TTTACGTCATATGATATGTTGGGAAGATTGGGAAGGCTGCTGCTGCTGCTGCTGCTGCT 504
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 Db 481 GTCTCAGACCAAGATCGAGCATCGAGCAGATACCCCGCGCGCGCGCGCGCGCGCGCGCG 540
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 Db 601 CCTGTTGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTGAACAGAGGT 660
 QY 684 TCAGACGCGCGGTGACCTCCAGAACAGGAGTGGGGCCATGTCGCCGATGTCATGGGAATC 743
 Db 661 TCAGACGCGCGGTGACCTCCAGAACAGGAGTGGGGCCATGTCGCCGATGTCATGGGAATC 720

QY 744 AGAGCATCTACCTCCGAAGCGTCTGATGGCGCGTCTTGGCTGGTGACACAGG 803
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 QY 804 CATCTACAGCGCTGGACTTGTCTCTCCAGGAAGGTAGCCAGCAGCTGTGAACACC 863
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 QY 864 AGCAGGAAGCCAGCGCTGAG 882
 Db 841 AGCAGGAAGCCAGCGCTGAG 859

RESULT 15
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 prime, mRNA sequence.
 ACCESSION AL517525
 VERSION AL517525
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 859)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 Bp 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 BASE COUNT 208 a 240 c 218 g 198 t 5 others
 ORIGIN

Query Match 47.8%; Score 812.6; DB 9; Length 859;
 Best Local Similarity 98.4%; Pred. No. 2.1e-128;
 Matches 847; Conservative 5; Mismatches 4; Indels 5; Gaps 3;

QY 729 GATGTCATGGAACTCAGACGATCTACCTCCGAAGCGTCTGATGGCGCGCTGTTGGC 788
 Db 859 GTTGTCATGGAACTCAGACGATCTACCTCCGAAGCGTCTGATGGCGCGCTGTTGGC 800
 QY 789 CTGTGGACCAAGCATCTACAGCGCTGGACTTGTGTTCTCTCCAGGAAGGTAGCCCA 848
 Db 799 CTGTGGACCAAGCATCTACAGCGCTGGACTTGTGTTCTCTCCAGGAAGGTAGCCCA 740
 QY 849 GCATGTGAAGACCCAGCAGGAGCCAGGCTGAGTGAACACAGACACCTGCTTCTGAA 908
 Db 739 GCATGTGAAGACCCAGCAGGAGCCAGGCTGAGTGAACACAGACACCTGCTTCTGAA 680

Sun Aug 18 12:47:10 2002

QY	909	CTCAAGCTGCGTTTATTAAATGCTCTCCCGCACAGCGCGGGCTTGGGCCCTGCACAGAT	968
Db	679	CTCAAGCTGCGTTTATTAAATGCTCTCCCGCACAGCGCGGGCTTGGGCCCTGCACAGAT	620
QY	969	ATTTCCTATTTCTTCTCTCACTATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCC	1028
Db	619	ATTTCCTATTTCTTCTCTCACTATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCT-C	561
QY	1029	TGCGGGAGTAGTTGGAAAGTTGGAAACCGTGTCCAGCACAGAAAGAAATGTGTCAGATGAG	1088
Db	560	TGCGGGAGTAGTTGGAAAGTTGGAAACCGTGTCCAGCACAGAAAGAAATGTGTCAGATGAG	501
QY	1089	CAGTCACACTGTTACTCCACAGCGGAGAGACCAGCTCAGAGGCCCCAGGAATCGGAGCGA	1148
Db	500	CAGTCACACTGTTACTCCACAGCGGAGAGACCAGCTCAGAGGCCCCAGGAATCGGAGCGA	441
QY	1149	AGCAGAGAGGTGGAACTGGGATTTGAACCCCGCCATCCTTCCACAGAGCCCATGCTC	1208
Db	440	AGCAGAGAGGTGGAACTGGGATTTGAACCCCGCCATCCTTCCACAGAGCCCATGCTC	381
QY	1209	AACCACTGTGGCGTTCTGTCGCCCTGCAGTTGGCAGAAAGATGTTTTGTCCTATTC	1268
Db	380	AACCACTGTGGCGTTCTGTCGCCCTGCAGTTGGCAGAAAGATG-TTTTGTCCCATTC	322
QY	1269	CTTGAGGCCACCGGACAGACTGGACACTAGGGTCAGGCGGGTGC--TGTGTGGG	1325
Db	321	CTTGAGGCCACCGGACAGACTGGACACTAGGGTCAGGCGGGTGC--TGTGTGGG	262
QY	1326	GAGAGCATGGCTGGGGTGGGGAGAGCTGTTGGCCGTGGTCCAGCTCTTGGCC	1385
Db	261	RAGAGCATGGCTGGGGTGGGGAGAGCTGTTGGCCGTGGTCCAGCTCTTGGCC	202
QY	1386	CCTGTGTAGTTGAGTCTCCTCTCTCAGACTGCTAAGTAGGGGCAGTGATGGTGGCAGG	1445
Db	201	CCTGTGTAGTTGAGTCTCCTCTCTCAGACTGCTAAGTAGGGGCAGTGATGGTGGCAGG	142
QY	1446	ACGAATTGAGATAATATCTCTGAGGTGCTGATGAGTGATTGACACACAGCACTCTCTAAA	1505
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QY	1506	TCTTCCTTGTGAGGATATGGGTCCGCAATCTACAGTTTCTTACTGTTTGTATCAAA	1565
Db	81	TCTTCCTTGTGAGGATATGGGTCCGCAATCTACAGTTTCTTACTGTTTGTATCAAA	22
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Db	21	ATCACTATCTTTCTGATAACA	1

Search completed: August 17, 2002, 01:10:14
Job time: 1979 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:25:50 ; Search time 60.78 seconds
(without alignments)
467.833 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VNAQPCRRGGILGLR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1299	99.8	256	AAW11894	MORT-1 modulator o
3	1047	80.4	208	AA131329	Human FADD protein
4	1040	79.9	208	AAW03653	FADD (Fas-associat
5	1040	79.9	208	AAW06154	Human FADD protein
6	1040	79.9	208	AAW06154	Human FADD prodona
7	1033	79.3	208	AAW06154	Human FADD. Homo
8	1028	79.0	208	AAW06154	Amino acid sequenc
9	985.5	75.7	201	AAW87492	Amino acid sequenc
10	982.5	75.5	201	AAW87491	Amino acid sequenc
11	719.5	55.3	205	AAW61900	Mouse apoptosis me

12	401	30.8	83	22	AAW84800	FADD death effecto
13	401	30.8	83	22	AAW61115	Human FADD DED1 do
14	375	28.8	81	19	AAW76623	Human FADD protein
15	370.5	28.5	117	22	AAW61902	Mouse apoptosis me
16	349	26.8	88	22	AAW61901	Mouse apoptosis me
17	318	24.4	62	17	AAW00210	Human MORT-1 prote
18	125.5	9.6	480	22	AAE06523	Mouse caspase 8 pr
19	122.5	9.4	239	22	ABB62302	Drosophila melanog
20	122	9.4	180	22	AAW84803	Human caspase 8 pr
21	122	9.4	180	22	AAW61118	Human Caspase-8.
22	122	9.4	220	19	AAW75961	MORT-1 binding pro
23	122	9.4	235	18	AAW11892	Cell death-associat
24	122	9.4	261	18	AAW31735	MACH isoform beta4
25	122	9.4	277	18	AAW11893	MACH isoform beta3
26	122	9.4	464	18	AAW11895	MACH isoform alpha
27	122	9.4	479	18	AAW31523	Interleukin-1 beta
28	122	9.4	479	18	AAW11891	MACH isoform alpha
29	122	9.4	479	19	AAW75963	Human Caspase-8.
30	122	9.4	479	22	AAE00605	Human Caspase-8.
31	122	9.4	479	22	AAW84812	Human caspase 8 L7
32	117	9.0	479	22	AAW84812	Human caspase 8 L7
33	117	9.0	479	22	AAW611127	Human Caspase-8 mu
34	117	9.0	479	22	AAW611128	Human Caspase-8 mu
35	117	9.0	291	21	AAW67420	Usurpin-gamma poly
36	116.5	8.9	1975	22	ABW52094	Drosophila melanog
37	116.5	8.9	81	19	AAW75962	Human Caspase-81.
38	116	8.9	83	22	AAW84796	Caspase 8 death ef
39	116	8.9	83	22	AAW61111	Human Caspase-8 DE
40	116	8.9	110	22	ABW30659	Peptide #3310 enco
41	116	8.9	110	22	ABW35830	Peptide #3336 enco
42	116	8.9	110	22	ABW21245	Protein #3244 enco
43	116	8.9	110	22	AAW56636	Human brain expres
44	116	8.9	110	22	AAW56636	Human bone marrow
45	116	8.9	110	22	AAW65013	

ALIGNMENTS

RESULT 1
AAW11894
ID AAW11894 standard; Protein: 256 AA.
XX
AC AAW11894;
XX
DT 29-OCT-1997 (first entry)
XX
DE Modulator of cellular toxicity (MORT-1).
XX
KW MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death;
KW antibody; Fas ligand receptor; Fas-R; death domain region; septic shock;
KW tumour necrosis factor; tumour; HIV-infection; oligodendrocyte death;
KW apoptosis/programmed cell death; p53-R; graft rejection; acute hepatitis;
KW autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;
KW TNF; therapy.
XX
OS Homo sapiens.
XX
PN WO9703998-A1.
XX
PD 06-FEB-1997.
XX
PF 14-JUN-1996; 96WO-US10521.
XX
PR 16-APR-1996; 96IL-0117932.
XX
PR 16-JUL-1995; 95IL-0114615.
XX
PR 17-AUG-1995; 95IL-0114986.
XX
PR 14-SEP-1995; 95IL-0115319.
XX
PR 27-SEP-1995; 95IL-0116586.
XX
PA (WEIN/) WEINWURZEL H.
XX
PA (YEDA) YEDA RES & DEV CO LTD.

PI Boldin M, Goltsev YV, Goncharov T, Wallach D;
 XX WPI: 1997-132570/12.
 DR N-PSDB; AAT61397.

XX New DNA encoding MACH protein that interacts with MORT-1 protein -
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.

XX PS Disclosure; Page 102-103; 163pp; English.

XX This sequence represents the mediator of cellular toxicity (MORT-1)
 CC protein. This sequence is bound by the protein of the invention (see
 CC AAW1892), designated MACH. MORT-1 binds to the FAS ligand receptor
 CC (FAS-R) death domain region, and triggers part of the cell death
 CC signalling cascade in mammalian cells. Vectors containing MACH, the MACH
 CC protein, and antibodies (Ab) against it are used to modulate the effect
 CC of FAS-R ligand or TNF on cells that carry FAS-R or p55-R. This is
 CC specifically for treating tumours, HIV-infected cells or other diseased
 CC cells, by control of apoptosis/programmed cell death. The MACH protein is
 CC a mediator of the cell death pathway initiated by TNF and FAS-R binding,
 CC i.e. it mimics or enhances the effect of MORT-1 where increased
 CC cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases
 CC of septic shock, graft rejection and acute hepatitis, sequences encoding
 CC antisense molecules or ribozymes, or Ab against MACH, are used.
 CC Compounds that inhibit MACH are potentially useful for controlling MACH
 CC activity e.g. in cases of autoimmune disease, oligodendrocyte death in
 CC multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can
 CC also be used to isolate and characterise other proteins and receptors
 CC involved in signalling and for Ab production. The Ab can be used to
 CC purify the new proteins and for diagnosis of conditions involving
 CC abnormal function of FAS-R mediated cellular effects.

XX Sequence 256 AA;

Query Match 100.0%; Score 1302; DB 18; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.3e-125;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRFGGILGLPKRRDLARASEPTREGARRAGPOPRPLADPAMPDFVLVLSHS 60
 DB 1 vnoapecrfggildglpkrrdlaraseptregarragpprpladpampdfvlvlhs 60
 QY 61 SLSSELTETKFLCIGRVVKKRLERVQSLDLFSLLEQNDLEPGHTELLRELLASLR 120
 DB 61 sllssseeltelkflcigrvvkkrlervqsgldlfsmlleqndlepghtellrelaslr 120
 QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDWRRRLAROLKVSdTIDIEDR 180
 DB 121 hdlrrvddfeagaaagapgeedlcaafnvicdnygkdwrrrlarolkvsdtkidsiedr 180
 QY 181 YPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLADLVQEVQOARDLQNRSGA 240
 DB 181 yprnltervreslrwktekenatvahlvglalrsqmnvladvlqvqvgardlqnrsga 240
 QY 241 MSPMSWNSDASTSEAS 256
 DB 241 mspmswnsdastseas 256

RESULT 2

ID AAR98346
 XX AAR98346 standard; Protein; 256 AA.

AC AAR98346;

XX DT 13-SEP-1996 (first entry)

XX MORT-1 modulator of FAS receptor.

XX MORT-1; HFL; FAS/APOL receptor; FAS-R; tumour; cancer; HIV;
 KW mediator of receptor toxicity; gene therapy.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 160..221
 FT /label= Death domain
 FT
 XX WO9618641-A1.
 PN
 XX 20-JUN-1996.
 PD
 XX 14-DEC-1995; 95WO-US16542.
 PF
 XX 16-JUL-1995; 95IL-0114615.
 PR
 XX 15-DEC-1994; 94IL-0112022.
 PR
 XX 19-FEB-1995; 95IL-0112692.
 PR
 XX (WEIN/) WEINWURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Boldin M, Mett I, Varfolomeev E, Wallach D;
 PI
 XX WPI: 1996-300569/30.
 DR N-PSDB; AAT30372.
 DR
 XX MORT-1 protein capable of interacting with FAS-R intracellular
 PT domain - useful for modulating FAS-R ligand effect on cells and
 PT treating, e.g. tumour cells and HIV-infected cells
 PT
 XX Claim 5; Fig 4; 73pp; English.
 PS
 XX MORT-1 (AAR98346) (Mediator of Receptor Toxicity), also designated HFL1,
 CC is a novel protein that binds to the intracellular domain (Fas-IC) of
 CC the FAS ligand receptor FAS-R (or FAS/APOL), and is capable of
 CC modulating the function of Fas-R. MORT-1 is also capable of
 CC self-association and can activate cell cytotoxicity on its own.
 CC Recombinant MORT-1 can be obtd. from host cells transformed with a
 CC vector carrying a cDNA clone (AAT30372) isolated from HeLa cells.
 CC MORT-1 can be used to modulate the FAS-R ligand on cells carrying
 CC an FAS-R. It can also be used to treat tumour cells or HIV-infected
 CC cells, or to raise antibodies.
 XX
 XX Sequence 256 AA;

Query Match 99.8%; Score 1299; DB 17; Length 256;
 Best Local Similarity 99.6%; Pred. No. 4.7e-125;
 Matches 255; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRFGGILGLPKRRDLARASEPTREGARRAGPOPRPLADPAMPDFVLVLSHS 60
 DB 1 vnoapecrfggildglpkrrdlaraseptregarragpprpladpampdfvlvlhs 60
 QY 61 SLSSELTETKFLCIGRVVKKRLERVQSLDLFSLLEQNDLEPGHTELLRELLASLR 120
 DB 61 sllssseeltelkflcigrvvkkrlervqsgldlfsmlleqndlepghtellrelaslr 120
 QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDWRRRLAROLKVSdTIDIEDR 180
 DB 121 hdlrrvddfeagaaagapgeedlcaafnvicdnygkdwrrrlarolkvsdtkidsiedr 180
 QY 181 YPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLADLVQEVQOARDLQNRSGA 240
 DB 181 yprnltervreslrwktekenatvahlvglalrsqmnvladvlqvqvgardlqnrsga 240
 QY 241 MSPMSWNSDASTSEAS 256
 DB 241 mspmswnsdastseas 256

RESULT 3
 ID AAY51329
 ID AAY51329 standard; Protein; 208 AA.

```

XX AC AAY51329;
XX DT 19-APR-2000 (first entry)
XX DE Human FADD protein.
XX KW FADD; human; antisense; inhibitor; Fas-associated death domain.
XX OS Homo sapiens.
XX PN US6015712-A.
XX PD 18-JAN-2000.
XX PF 19-JUL-1999; 99US-0357072.
XX PR 19-JUL-1999; 99US-0357072.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Cowsett LM, Baker BF, Zhang H;
XX WPI; 2000-126316/11.
XX DR N-PSDB; AAZ44745.
XX PT Antisense oligonucleotides, useful for inhibiting human Fas-associated
XX death domain (FADD) expression are targeted to the 3' untranslated
XX region of the FADD gene.
XX PS Example 13; Column 43-46; 37pp; English.
XX CC This invention describes novel antisense oligonucleotides (OGNs) (I)
XX 8-20 nucleotides in length that specifically hybridize with and inhibit
XX nucleic acids encoding human Fas-associated death domain (FADD),
XX targeted to the 3' untranslated region (3'UTR). (I) can be used to treat
XX animals, especially humans, suspected of having or being prone to a
XX disease or condition associated with FADD expression. This sequence
XX represents the human FADD protein described in the method of the
XX invention.
XX SQ Sequence 208 AA;

Query Match 80.4%; Score 1047; DB 21; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 MDPLVLHVSLSLSSELTELKFLCLGRVVRKKLERVQSLDLFSMLLEQNLDLEPGHT 108
DB 1 mdplvlhvselsseitelkflclgrvvrkklervgsgldlfsmlleqndlepght 60
QY 109 ELRLRELLASLRHDLRRVDDFAGAAAGAAPGEEDLCRAFNVICDVGKDWRLARQLK 168
DB 61 ellrellaslrhdlrrvdvdfagaaagapgeedlcaafnvicdvnvgkdwrlarqlk 120
QY 169 VSDTKIDSIEDYPRNTERVRESLRIRWKNTEKENATVAHLVGLRSCQMNVLVADLVQEV 228
DB 121 vsdtkidsiedyprnltervreslrirwknntekenatvahlvgalscqmnlvadvlvqev 180
QY 229 QQARDLQNRSGAMPKSNWSDASTSEAS 256
DB 181 qqardlqnrsgampkswnsdastseas 208

RESULT 4
ID AA003653
XX AC AA003653;
XX DT 22-FEB-1997 (first entry)

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DE XX FADD (Fas-associating protein with novel death domain) protein.
KW XX Human; FADD; Fas-associating protein with novel death domain;
KW XX apoptosis; Fas receptor; death domain; gene therapy; antibody;
KW XX immunosassay; drug screening; diagnostic; AIDS; antiinflammatory;
KW XX antitumour; cerebroprotective; neuroprotective.
OS XX Homo sapiens.
XX FH Key
XX FT Region 1..125 Location/Qualifiers
FT FT /note= "N-terminal fragment, inducing apoptosis but
FT FT not binding to Fas receptor"
FT FT Region 35..208
FT FT /note= "C-terminal active fragment"
FT FT Region 41..208
FT FT /note= "C-terminal active fragment"
FT FT Region 42..208
FT FT /note= "Fas receptor-binding NFD-2 polypeptide"
FT FT Region 61..208
FT FT /note= "Fas receptor-binding NFD-3 polypeptide"
FT FT Region 80..208
FT FT /note= "Fas receptor-binding NFD-4 polypeptide"
FT FT Misc-difference 121
FT FT /note= "Altered to Asn in FADDmt mutant"
FT FT Domain 111..177
FT FT /note= "Death domain"
XX PN W09631603-A2.
XX XX 10-OCT-1996.
XX PF 28-FEB-1996; 96WO-US02857.
XX PR 18-MAY-1995; 95US-0443982.
XX PR 03-APR-1995; 95US-0416379.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Dixit VM, O'Rourke K;
XX DR WPI: 1996-465026/46.
XX DR N-PSDB; AAT39397.
XX PT FADD protein that binds to cytoplasmic region of Fas receptor - for
XX identifying inhibitors of Fas-associated apoptosis useful for
XX treating e.g. AIDS, leukaemia, stroke, etc
XX PS Example 1; Fig 2A-B; 96pp; English.
XX CC The sequence corresponds to FADD (Fas-associating protein with novel
XX death domain), which binds the cytoplasmic region of a Fas receptor,
XX and modulates apoptosis induced by activation of the receptor by
XX ligand binding. The FADD cDNA has been isolated using a yeast
XX two-hybrid system to screen for proteins interacting with the Fas
XX cytoplasmic domain. The protein contains a death domain, with
XX interacts with the death domain of Fas. Mutation of Val-121 to
XX Asn in mutant FADDmt disrupts binding and/or signalling properties.
XX C-terminal polypeptides NFD-2, NFD-3 and NFD-4 bind the Fas receptor
XX cytoplasmic domain in vitro. An N-terminal fragment induces
XX apoptosis but does not bind the Fas receptor. The encoding DNA may
XX be used in gene therapy, and the protein or a corresponding antibody
XX may be used to screen for agents modulating FADD pathway cellular
XX functions and Fas-associated apoptosis, for use in therapy of e.g.
XX AIDS, inflammation, leukaemia, myocardial infarction, degenerative
XX disease, etc.
XX SQ Sequence 208 AA;

```

Query Match 79.9%; Score 1040; DB 17; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC probes that identify wild-type or mutant coding sequences. They are
 CC also useful for expressing FIP mRNA, proteins or fusion proteins,
 CC and in the generation of FIP antisense oligonucleotides and
 CC ribozymes. They are also useful in expression constructs and in
 CC gene delivery vehicles (optionally in combination with a condensing
 CC agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
 CC (including variants), FIP-specific ribozymes or single-chain
 CC antibodies into eukaryotic cells. This is the human FADD protein.
 CC Human FIP protein binds to amino acids 1-110 of this sequence.
 XX
 SQ Sequence 208 AA;

 Query Match 79.9%; Score 1040; DB 20; Length 208;
 Best Local Similarity 99.5%; Pred. NO. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 49 MDPLVLLHSVSSLSSELTCLKFICLGRVVKRKIERVQSGDLDFSMLEQNDLEPGHT 108
 Db 1 mdplvllhsvsslsseletkfcigrvgrkiervqsgdlfsmleqndlepght 60

 QY 109 ELIRELLASLRHDLRRVDDFAGAAAGAPGEEDLCAAFNVICDNVGDWRRLARQLK 168
 Db 61 ellirellaslrhdlrrvddfeagaaagapeeedlcaafnvicdnvgkdwrrlarqlk 120

 QY 169 VSDTKIDSIEDRYPRNLTERVRESLRIRWNTKENATVAHLVGALRSCQNMNVADLVQEV 228
 Db 121 vsdtkidsiedryprnltervreslrirwntekenatvahlvgalrscqnmnvadlvqev 180

 QY 229 QQARDLQNRSGAMSPMWSNDASTSEAS 256
 Db 181 qqardlqnrsgamspmwnsdastseas 208

 RESULT 5
 AAW96154
 ID AAW96154 standard; Protein; 208 AA.
 XX
 AC AAW96154;
 XX
 DT 27-APR-1999 (first entry)
 XX
 DE Human FADD protein.
 XX
 KW FIP; FADD interacting protein; FADD; Fas-associated protein with a
 KW novel death domain; cell death; apoptosis; Alzheimer's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; muscular dystrophy;
 KW amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasma;
 KW protozoa; neoplasia; dysplasia; hyperplasia.
 XX
 OS Homo sapiens.
 XX
 PN WO9900499-A1.
 XX
 PD 07-JAN-1999.
 XX
 PF 26-JUN-1998; 98WO-US13320.
 XX
 PR 03-JUN-1998; 98US-0087986.
 PR 26-JUN-1997; 97US-0050792.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Chen TT, Williams LT;
 XX
 XX WPI; 1999-095745/08.
 DR N-PSDB; AAX08910.
 XX
 XX New FADD (Fas-associated protein with a novel death
 PT domain)-interacting protein - useful for inducing or preventing
 PT apoptosis in a cell, to aid in controlling apoptosis-related
 PT diseases
 XX
 PS Disclosure; Page 47; 58pp; English.
 XX
 CC An epitope of human FADD (Fas-associated protein with a novel
 CC death domain)-interacting protein (FIP protein) comprising amino
 CC acids 348-727 of the protein described in AAW96153, can be used to
 CC induce or prevent apoptosis in a cell. Specifically, decreasing the
 CC levels of FIP348-727 prevents apoptosis. This is useful in cells
 CC which are dying prematurely, eg: Alzheimer's disease, Acquired
 CC Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic
 CC lateral sclerosis (and other muscle wasting diseases), autoimmune
 CC diseases, and diseases where cells are infected with a pathogen
 CC (virus, bacteria, fungus, mycoplasma or protozoa). Increasing the
 CC levels of FIP 348-727 induces apoptosis which is useful in cells
 CC suffering from neoplasias, dysplasias, hyperplasias, or their
 CC symptoms. Purified and isolated FIP subgenomic polynucleotides are
 CC useful as primers to obtain more copies of the nucleotides, and as

CC probes that identify wild-type or mutant coding sequences. They are
 CC also useful for expressing FIP mRNA, proteins or fusion proteins,
 CC and in the generation of FIP antisense oligonucleotides and
 CC ribozymes. They are also useful in expression constructs and in
 CC gene delivery vehicles (optionally in combination with a condensing
 CC agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
 CC (including variants), FIP-specific ribozymes or single-chain
 CC antibodies into eukaryotic cells. This is the human FADD protein.
 CC Human FIP protein binds to amino acids 1-110 of this sequence.
 XX
 SQ Sequence 208 AA;

 Query Match 79.9%; Score 1040; DB 20; Length 208;
 Best Local Similarity 99.5%; Pred. NO. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 49 MDPLVLLHSVSSLSSELTCLKFICLGRVVKRKIERVQSGDLDFSMLEQNDLEPGHT 108
 Db 1 mdplvllhsvsslsseletkfcigrvgrkiervqsgdlfsmleqndlepght 60

 QY 109 ELIRELLASLRHDLRRVDDFAGAAAGAPGEEDLCAAFNVICDNVGDWRRLARQLK 168
 Db 61 ellirellaslrhdlrrvddfeagaaagapeeedlcaafnvicdnvgkdwrrlarqlk 120

 QY 169 VSDTKIDSIEDRYPRNLTERVRESLRIRWNTKENATVAHLVGALRSCQNMNVADLVQEV 228
 Db 121 vsdtkidsiedryprnltervreslrirwntekenatvahlvgalrscqnmnvadlvqev 180

 QY 229 QQARDLQNRSGAMSPMWSNDASTSEAS 256
 Db 181 qqardlqnrsgamspmwnsdastseas 208

 RESULT 6
 AAB84804
 ID AAB84804 standard; Protein; 208 AA.
 XX
 AC AAB84804;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE Human FADD prodomain.
 XX
 KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
 XX
 OS Homo sapiens.
 XX
 PN US6207458-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 07-MAY-1998; 98US-0074044.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Chaudhary PM, Hood L;
 XX
 XX WPI; 2001-342087/36.
 DR
 XX
 PT Testing candidate compound affecting cellular NF-kappaB JNK, apoptosis
 PT activity by comparing cell activity in presence and absence of
 PT proteinaceous species having two death effector domain and test
 PT compound -
 XX
 PS Disclosure; Column 51-52; 62pp; English.
 XX
 CC The present invention relates to testing candidate compounds to
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
 CC The method involves the use of 2 death effector domains (DED). The
 CC compounds identified by the invention have therapeutic

CC applications and are useful for regulating cellular NF-kappaB, JNK
 CC and apoptosis activity. The assay is useful for identifying
 CC pharmacological agents or lead compounds generally involved in
 CC assaying for compounds which regulate or modulate a cell activity.
 CC The present sequence is a prodomain used in the invention.

XX Sequence 208 AA;

Query Match 79.9%; Score 1040; DB 22; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCLGRVVKRLERVSQGLDLFSMLLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslsesselteklfclgrvgrkrlervqsgldlfsmlleqndlepght 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDVGKDWRRRLARQLK 168
 DB 61 ellrellaslrhdlrrvddfeagaaagaeedlcaafnvicdvgkdwrrrlarqlk 120
 QY 169 VSDTKIDSTEDRYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLVADLVQEV 228
 DB 121 vsdtkidsiedryprnltervreslrwktekenatvahlvgalsrcqmnlvadvlqv 180
 QY 229 QQARDLQNRSGAMSPMNSDASTSEAS 256
 DB 181 qqardlqnrsgamspmswnsdastseas 208

RESULT 7
 AAB61119
 ID AAB61119 standard; protein; 208 AA.
 AC AAB61119;
 DT 02-MAY-2001 (first entry)
 DE Human FADD.
 KW Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KW Jun N-terminal kinase; JunK; apoptosis; Caspase-8 mutant.
 OS Homo sapiens.
 PN US6160095-A.
 PD 12-DEC-2000.
 PF 24-AUG-1999; 98US-0382155.
 PR 07-MAY-1998; 98US-0074044.
 PA (UNIW) UNIV WASHINGTON.
 PA (STOW-) STOWERS INST MEDICAL RES.
 PI Hood L, Chaudhary PM;
 DR WPI; 2001-101569/11.
 PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
 PT for therapeutic purposes -
 PS Example 8; Fig 11; 60pp; English.
 CC The present sequence has been shown to regulate the nuclear factor-kappa
 CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It
 CC is provided in a specification relating to novel mutants (D73A, L74A and
 CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
 CC and apoptosis activities. The Caspase-8 mutants are useful for
 CC therapeutic purposes and in test methods or assays for determining
 CC whether a candidate compound has a significant effect upon cell

CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the
 CC discovery and/or design of therapeutic agents.

XX Sequence 208 AA;

Query Match 79.3%; Score 1033; DB 22; Length 208;
 Best Local Similarity 99.0%; Pred. No. 7.5e-98;
 Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCLGRVVKRLERVSQGLDLFSMLLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslsesselteklfclgrvgrkrlervqsgldlfsmlleqndlepght 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDVGKDWRRRLARQLK 168
 DB 61 ellrellaslrhdlrrvddfeagaaagaeedlcaafnvicdvgkdwrrrlarqlk 120
 QY 169 VSDTKIDSTEDRYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLVADLVQEV 228
 DB 121 vsdtkidsiedryprnltervreslrwktekenatvahlvgalsrcqmnlvadvlqv 180
 QY 229 QQARDLQNRSGAMSPMNSDASTSEAS 256
 DB 181 qqardlqnrsgamspmswnsdastseas 208

RESULT 8
 AAW87493
 ID AAW87493 standard; Protein; 208 AA.
 AC AAW87493;
 DT 12-FEB-1999 (first entry)
 DE Amino acid sequence of MORT1 Isoform MORT1G173A from human brain.
 KW MORT1; MORT1del21; NTERA2; CNS; Isoform: death domain; Fas/APOL;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.
 OS Homo sapiens.
 PN WO9849297-A1.
 PD 05-NOV-1998.
 PF 14-APR-1998; 98WO-US07439.
 PR 25-APR-1997; 97US-0044835.
 PA (AMHP) AMERICAN HOME PROD CORP.
 PI Bingham BW, Birsan C, Wood AT, Young KH;
 DR WPI; 1999-009424/01.
 DR N-PSDB; AAV71930.
 PT Human, neuronal MORT1 isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 PS Claim 7; Pages 30-31; 31pp; English.
 CC This represents the amino acid sequence of a MORT1 isoform MORT1G173A.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209019. The cDNA has a nucleotide substitution (G
 CC to A) at basepair position 173 of the published MORT1 coding sequence.
 CC The invention relates to three MORT1 nucleic acid isoforms (AAV71928 to
 CC AAV71930) that encode proteins which can interact with the death domain
 CC of Fas/APOL. The MORT1 isoforms can also interact with MACH alpha1 or
 CC other members of the ICE/Ced3 (caspase) family of proteins. The
 CC transcript isoforms, together with their encoded proteins are useful as

CC screening agents in diagnosing CNS diseases, and in discovering
 CC CNS-specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.
 XX
 SQ Sequence 208 AA;

Query Match 79.0%; Score 1028; DB 20; Length 208;
 Best Local Similarity 98.6%; Pred. No. 2.5e-97;
 Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSSSSELTEKLCGRVVKRKLKRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslseseltelkclgrvgrklervqsgdlfsmileqndlepeht 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNVKGDKWRRLARQLK 168
 DB 61 ellrellaslrhdlrrvddfeagaaagapgeedlcaafnvicdnvkgdkwrrlarqlk 120
 QY 169 VSDTKIDSIDRYPRNLTERVRESLRWKNTKENATVAHLVGLRSCOMNLVADLVQEV 228
 DB 121 vadtksidsiedryprnltervreslrwknktenatvahlvglrscqmnlaadlvgev 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 qqardlqnrsgamspmswnsdastseas 208

RESULT 9

AAW87492
 ID AAW87492 standard; Protein; 201 AA.

XX AAW87492;

DT 12-FEB-1999 (first entry)

DE Amino acid sequence of MORT1 isoform MORT1del21 from human brain.

KW MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/AP01;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.

XX Homo sapiens.

XX WO9849297-A1.

XX 05-NOV-1998.

XX 14-APR-1998; 98WO-US07439.

XX 25-APR-1997; 97US-0044835.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Bingham BW, Birsan C, Wood AT, Young KH;

XX WPI; 1999-009424/01.

XX N-PSDB; AAV71929.

PT Human, neuronal MORT1 iso:form(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds

XX Claim 6; Pages 28-29; 31pp; English.

CC This represents the amino acid sequence of a MORT1 isoform MORT1del21.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209018. The cDNA has a 21 base pair deletion as
 CC compared to the published MORT1 sequence (Op 172-192 of the coding
 CC sequence). The invention relates to three MORT1 nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the

CC death domain of Fas/AP01. The MORT1 isoforms can also interact with MACH
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.
 XX
 SQ Sequence 201 AA;

Query Match 75.7%; Score 985.5; DB 20; Length 201;
 Best Local Similarity 95.7%; Pred. No. 5.5e-93;
 Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPFLVLLHSVSSSSSELTEKLCGRVVKRKLKRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslseseltelkclgrvgrklervqsgdlfsmileqndlep--- 57
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNVKGDKWRRLARQLK 168
 DB 58 ----ellaalrrhdlrrvddfeagaaagapgeedlcaafnvicdnvkgdkwrrlarqlk 113
 QY 169 VSDTKIDSIDRYPRNLTERVRESLRWKNTKENATVAHLVGLRSCOMNLVADLVQEV 228
 DB 114 vadtksidsiedryprnltervreslrwknktenatvahlvglrscqmnlaadlvgev 173
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 174 qqardlqnrsgamspmswnsdastseas 201

RESULT 10

AAW87491

ID AAW87491 standard; Protein; 201 AA.

XX AAW87491;

DT 12-FEB-1999 (first entry)

DE Amino acid sequence of MORT1 isoform MORT1del21 from NTERA2 cells.

KW MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/AP01;

KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;

KW in vivo agent; neuronal apoptosis; human.

XX Homo sapiens.

XX WO9849297-A1.

XX 05-NOV-1998.

XX 14-APR-1998; 98WO-US07439.

XX 25-APR-1997; 97US-0044835.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Bingham BW, Birsan C, Wood AT, Young KH;

XX WPI; 1999-009424/01.

XX N-PSDB; AAV71928.

PT Human, neuronal MORT1 iso:form(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds

XX Claim 5; Pages 26-27; 31pp; English.

CC This represents the amino acid sequence of a MORT1 isoform MORT1del21.
 CC The encoding cDNA was isolated from NTERA2 cells and deposited under the
 CC accession number ATCC 209013. The cDNA has a 21 base pair deletion as

Sun Aug 18 12:47:10 2002

CC compared to the published MOR1 sequence (bp 172-192 of the coding
CC sequence). The invention relates to three MOR1 nucleic acid isoforms
CC (AAV71928 to AAV71930) that encode proteins which can interact with the
CC death domain of Fas/CD95. The MOR1 isoforms can also interact with MACH
CC alpha or other members of the ICE/Ced3 (Caspase) family of proteins.
CC The transcript isoforms, together with their encoded proteins are useful
CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
CC specific anti-apoptotic compounds. They are useful in gene therapy
CC either as in vivo agents in humans or as experimental tools in
CC manipulating neuronal apoptosis in cell culture and animal model
CC systems.

SQ Sequence 201 AA;
Query Match 75.5%; Score 982.5; DB 20; Length 201;
Best Local Similarity 95.7%; Pred. No. 11e-92;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCLGRVYVKKLRRVQSGDLFSMLLEQNDLEPGHT 108
DB 1 mdpflvllhsvsslsselelklfclgrvyrkkrlerqvsgldlfsmlleqndlepght 57

QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGPGEEDLCAAFNVICDNGKDWRLRLARQLK 168
DB 58 ----ellaslrrhdlrrvddfeagaaagpgeedlcaafnvicdngkdwrlrlarqlk 113

QY 169 VSDTKIDSIEDRYPRNLTERVRESLRIMKTEKENATVAHLVGALRSCOMNLVADLVQEV 228
DB 114 vsdtkidsiedryprnltervreslriwntekenatvahlvgalrscomnlvadlvqev 173

QY 229 QQARDLQNRGAMSPMSWNSDASTSEAS 256
DB 174 qqardlqnrsgamspmswnsdastseas 201

RESULT 11
AAB61900
ID AAB61900 standard; Protein: 205 AA.
AC AAB61900;
DT 08-MAY-2001 (first entry)
DE Mouse apoptosis mediator FADD.
KW FADD; DED; FADD-DED; death effector domain; apoptosis mediator;
KW bacterial; cell death; reactive oxygen species; ROS; mouse.
OS Mus sp.
PN WO200104153-A1.
PD 18-JAN-2001.
PF 11-JUL-2000; 2000WO-KR00721.
PR 12-JUL-1999; 99KR-0027964.
PA (IMAG-) IMAGENE CO LTD.
PI Kim S, Kim K;
PS WPI; 2001-138318/14.
DR N-PSDB; AAC85064.
XX Novel death effector domain of mammalian apoptosis mediator, for
XX inducing bacterial and mammalian cell death by enhancing cellular level
XX of reactive oxygen species
XX Claim 1; Page 43-44; 47pp; English.
XX The invention relates to a death effector domain (DED) of a mammalian

CC apoptosis mediator (FADD). The FADD-DED induces bacterial and mammalian
CC cell death by enhancing cellular level of Reactive Oxygen Species (ROS).
CC The present sequence represents a mouse FADD, a pro-apoptotic mediator
CC consisting of N-terminal death effector domain (DED) and C-terminal death
CC domain (DD).
CC Sequence 205 AA;
Query Match 55.3%; Score 719.5; DB 22; Length 205;
Best Local Similarity 68.4%; Pred. No. 1.2e-65;
Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCLGRVYVKKLRRVQSGDLFSMLLEQNDLEPGHT 108
DB 1 mdpflvllhsvsslsselelklfclgrvyrkkrlerqvsgldlfsmlleqndlepght 60

QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGPGEEDLCAAFNVICDNGKDWRLRLARQLK 168
DB 61 gllrellaslrrhdlrrvddfeagaaagpgeedlcaafnvicdngkdwrlrlarelk 120

QY 169 VSDTKIDSIEDRYPRNLTERVRESLRIMKTEKENATVAHLVGALRSCOMNLVADLVQEV 228
DB 121 vseakmdgieekyprlservreslriwntekenatvahlvgalrscomnlvadlvqev 180

QY 229 QQARDLQNRGAMSPMSWNSDASTSE 254
DB 181 qes---vaksenmpvlrdstvsse 203

RESULT 12
AAB84800
ID AAB84800 standard; Protein: 83 AA.
AC AAB84800;
DT 12-JUL-2001 (first entry)
DE FADD death effector domain 1.
KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
KW Homo sapiens.
OS US6207458-B1.
PN 27-MAR-2001.
PD 07-MAY-1998; 98US-0074044.
PR 07-MAY-1998; 98US-0074044.
PA (UNIW) UNIV WASHINGTON.
PI Chaudhary PM, Hood L;
PS WPI; 2001-342087/36.
XX Testing candidate compound affecting cellular NF-kappaB JNK, apoptosis
XX activity by comparing cell activity in presence and absence of
XX proteinaceous species having two death effector domain and test
XX compound -
XX Claim 10; Column 45-47; 62pp; English.
XX The present invention relates to testing candidate compounds to
XX determine whether they affect NF-kappaB, JNK and apoptosis activity.
XX The method involves the use of 2 death effector domains (DED). The
XX compounds identified by the invention have therapeutic
XX applications and are useful for regulating cellular NF-kappaB, JNK
XX and apoptosis activity. The assay is useful for identifying
XX pharmacological agents or lead compounds generally involved in
XX assaying for compounds which regulate or modulate a cell activity.

CC The present sequence is a death effector domain of the invention.
XX
SQ Sequence 83 AA;

Query Match 30.8%; Score 401; DB 22; Length 83;
Best Local Similarity 98.8%; Pred. No. 1.8e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLVHVSLSSELTELKFLCGRVYVKKLKVQSGDLFMSMLLEQNDLEPGHT 108
DB 1 mdpflvllhsvsslssesteltklcgrvgrgkrklervqsgldlfsmlleqndlepght 60
QY 109 ELLRELLASLRHDLRRVDDFE 131
DB 61 ellrellaslrhdlrrvddfe 83

RESULT 13
AAB61115
ID AAB61115 standard; protein; 83 AA.
XX
AC AAB61115;

DT 02-MAY-2001 (first entry)
XX Human FADD DED1 domain.
DE
KW Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
KW Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant;
KW death effector domain; DED.

XX Homo sapiens.
OS
XX
XX US6160095-A.
PN
XX 12-DEC-2000.
PD
XX 24-AUG-1999; 99US-0382155.
PF
XX 07-MAY-1998; 98US-0074044.
PR
XX (UNIW) UNIV WASHINGTON.
PA
PA (STOW-) STOWERS INST MEDICAL RES.

PI Hood L, Chaudhary PW;
XX
XX WPI; 2001-101569/11.
DR
XX Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
PT for therapeutic purposes -
XX Example 8; Fig 11; 60pp; English.

CC The present sequence is a death effector domain (DED) of a protein
CC that has been shown to regulate the nuclear factor-kappa
CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It
CC is provided in a specification relating to novel mutants (D73A, L74A and
CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
CC and apoptosis activities. The Caspase-8 mutants are useful for
CC therapeutic purposes and in test methods or assays for determining
CC whether a candidate compound has a significant effect upon cell
CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the
CC discovery and/or design of therapeutic agents.

XX
SQ Sequence 83 AA;
Query Match 30.8%; Score 401; DB 22; Length 83;
Best Local Similarity 98.8%; Pred. No. 1.8e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLVHVSLSSELTELKFLCGRVYVKKLKVQSGDLFMSMLLEQNDLEPGHT 108
DB 1 mdpflvllhsvsslssesteltklcgrvgrgkrklervqsgldlfsmlleqndlepght 60
QY 109 ELLRELLASLRHDLRRVDDFE 131
DB 61 ellrellaslrhdlrrvddfe 83

RESULT 14
AAW76623
ID AAW76623 standard; protein; 81 AA.
XX
AC AAW76623;
XX
DT 12-JUL-1999 (first entry)
XX
DE Human FADD protein fragment containing death effector domain.
KW Death effector domain; human; murine; anti-apoptotic; treatment;
KW HIV infection; autoimmune disease; FADD protein.

XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= unknown
FT
XX DE19713393-A1.
PN
XX 08-OCT-1998.
PD
XX 01-APR-1997; 97DE-1013393.
PF
XX 01-APR-1997; 97DE-1013393.

PR
XX (TSCH/) TSCHOPP J.
PA (APOT-) APOTTECH SA.
XX
XX Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;
PI Irmeler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;
PI Thome M, Tschoopp J, Hofmann K;
XX
XX WPI; 1998-532710/46.
DR
XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases
PT
XX Disclosure; Fig 2; 45pp; German.

XX
XX This invention describes novel human and mouse anti-apoptotic gene
CC products which contain at least one death effector domain. The products
CC of the invention are used in the treatment of HIV infections and
CC autoimmune diseases.

XX SQ Sequence 81 AA;

Query Match 28.8%; Score 375; DB 19; Length 81;
Best Local Similarity 95.1%; Pred. No. 8.1e-31;
Matches 77; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPLVLVHVSLSSELTELKFLCGRVYVKKLKVQSGDLFMSMLLEQNDLEPGHT 108
DB 1 mdpalxllhsvsslssesteltklcgrvgrgkrklervqsgldlfsmlleqndlepght 60
QY 109 ELLRELLASLRHDLRRVDD 129
DB 61 ellrellaslrhdlrrvdd 81

RESULT 15
AAB61902

Search completed: August 17, 2002, 00:37:08
Job time: 678 sec

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Sequence 2, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 1, Appl

ALIGNMENTS

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1
RESULT
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; Sequence 1, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowserst
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 1
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(771)
; US-09-357-072-1

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DB				
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QY				
DB				
61	CGAGACCTTGGCCAGGGCCACGAGCCCGAGACAGAGGGCCGCGGAGGCCGGCGCGCAG	120		
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DB				
61	cgaaccccgccagggccagcgagccgagagagggcgcgaggggccggcgcaag	120		
QY				
DB				
121	CCCCGGCCGCTTGAGACACCGCCCATGGACCCGTTCTGGTGTGTGTGCACTCGGGTGTCG	180		
QY				
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121	ccccggccgcttgcaagcccgccatggacccttccctggctgtctgctacctcgggtgtcg	180		
QY				
DB				
181	TCCAGCCTGTGCAGCAGCGAGCTCACCAGAGCTCAAGTTCCTATGCTTCGGGGCGGTGGTC	240		
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DB				
181	tccagccctgcagacagcgagctgaaccgagctcaagttcctaigtctcggcggtcggttc	240		
QY				
DB				
241	AAGCGCAAGCTTGGAGCGCGTGCAGAGGGGCTTAGACCTCTTCTCCATGTGCTGGAGCAG	300		
QY				
DB				
241	aagcgcaagcttggagcgcggtgcagagcggcctagaccctctcccatgtctcgtctggagcag	300		
QY				
DB				
301	AACGACCTTGGACCCCGGCGCACCGAGCTCTCTGGCGAGCTGTTCGCGCTCCCTTCGCGCCG	360		
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DB				

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now nucleic - nucleic search, using sw model

Run on: August 17, 2002, 00:39:00 ; Search time 54.76 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

searched: 383533 seqs, 122816752 residues

total number of hits satisfying chosen parameters: 767066

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minimum DB seq length: 0

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 2
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Post-processing:	Minimum	Maximum	Match	Use
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Maximum Match 1000
Listing first 45 summaries

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5: /cgn2_6/pdodata/1/ins/PCTUS_COMB.seq
6: /cgn2_6/pdodata/1/ins/backfiles1.seq

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, \bar{p} is the average of the \bar{p} 's determined by analysis of the total score distribution.

SUMMARIES

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2	1701	100.0	1701	5	PCT-US95-16542-1
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4	620.6	36.5	627	4	US-09-064-414-5
5	571.8	33.6	606	4	US-09-064-414-1
6	570.2	33.5	606	4	US-09-064-414-3
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8	52.6	3.1	68750	4	US-09-568-102-1
9	52.6	3.1	68750	4	US-09-567-969-1
10	52.6	3.1	68750	4	US-09-568-480-1
11	52.6	3.1	68750	4	US-09-568-486-1
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15	49.6	2.9	2961	2	US-08-407-875-1
16	49.4	2.9	5437	1	US-07-661-610C-1
17	49.2	2.9	30001	2	US-08-125-468-1
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22	49	2.9	2635	3	US-09-126-280-3
23	49	2.9	2670	3	US-09-126-280-3
24	48.4	2.8	4695	2	US-08-231-193A-57
25	48.4	2.8	4695	2	US-08-486-273A-57
26	48.4	2.8	4695	3	US-08-940-086A-57
27	48	2.8	4695	4	US-08-940-036A-57

Db 301 aacgaacctggagcccgccgagccgagctcctgctgagagctgctgctcctccctgcccgc 360
Qy 361 CACGACCTGCTGCGCGCGCTGCGAGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCT 420
Db 361 cagcactgtctgcccgcgctgcagcacttcgagcagcagcagcagcagcagcagcagc 420
Qy 421 GGGGAAGAACAGCCTGTGTGAGCATTAACTGATGATGATGATGATGATGATGATGATG 480
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Qy 601 AAGGAGAACCAACAGTGGCCACCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCG 660
Db 601 aaggagaaagcaacagtggccacactgtgagcagcagcagcagcagcagcagcagc 660
Qy 661 GTGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Qy 1081 CAGATGAGCAGTCACTGCTTACTTCCACGCGGAGGAGCAGCTGAGGAGGAGGAGGAG 1140
Db 1081 cagatgagcagtcacactgttacttccacagcagcagcagcagcagcagcagcagc 1140
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Qy 1261 CCATTTCTTGGAGCCACCGGAGCAGACTGGACCTGAGCTAGGCTAGGCTAGGCTAGG 1320
Db 1261 cccatttcttggagccacccggagacaccccgacactgagcagcagcagcagcagcag 1320
Qy 1321 GTGGGAGAGGATGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 gttgggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1380
Qy 1381 TGGCCCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1440
Db 1381 tggccctgtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1440

RESULT 2

PCT-US95-16542-1
; Sequence 1, Application PC/TUS9516542
; GENERAL INFORMATION:
; APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
; APPLICANT: WEINMURZEL, Henry
; APPLICANT: WALLACH, David
; APPLICANT: BOLDIN, Mark
; APPLICANT: VARFOLOMEV, Eugene
; APPLICANT: METT, Igor
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16542
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 112022
; FILING DATE: 15-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 112692
; FILING DATE: 19-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114615
; FILING DATE: 16-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1701 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..768
PCT-US95-16342-1

Query Match
Best Local Similarity 100.0%; Score 1701; DB 5; Length 1701;
Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAATCAGGACCGGAGTGCAGGTTCCGGGGTGGAAATCCTTGGGCGCGTGGGCAAGCGG 60
DB 1 GTGAATCAGGACCGGAGTGCAGGTTCCGGGGTGGAAATCCTTGGGCGCGTGGGCAAGCGG 60
QY 61 CGAGACCTGCCAGGCGCCAGGCGGAGGAGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGG 120
DB 61 CGAGACCTGCCAGGCGCCAGGCGGAGGAGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGG 120
QY 121 CCCGGCGCGTTCGACAGCCCGCCATGACCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 CCCGGCGCGTTCGACAGCCCGCCATGACCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 TCCAGGCTGTGAGAGCGGAGTGCAGGCTCAAGTTCCCTATGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 TCCAGGCTGTGAGAGCGGAGTGCAGGCTCAAGTTCCCTATGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AAGCGCAAGCTGGAGCGGCTGCAGAGCGGCTGACGCGGCTGACCTCTCTCCATGCTGCGAG 300
DB 241 AAGCGCAAGCTGGAGCGGCTGCAGAGCGGCTGACGCGGCTGACCTCTCTCCATGCTGCGAG 300
QY 301 AACGACCTGGAGCGCGGCGACCGAGCTCCTGCGGAGCTGCTGCGGCGGCGGCGGCGGCGGCT 360
DB 301 AACGACCTGGAGCGCGGCGACCGAGCTCCTGCGGAGCTGCTGCGGCGGCGGCGGCGGCGGCT 360
QY 361 CACGACCTGCTGCGGCGGCTGCGAGCTTTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 420
DB 361 CACGACCTGCTGCGGCGGCTGCGAGCTTTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 420
QY 421 GGGGAAGAACCTGTGTGAGGATTTACGTCATATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 GGGGAAGAACCTGTGTGAGGATTTACGTCATATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 AGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 AGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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DB 661 GTGGCTGACCTGTGACAGAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 720
QY 721 ATGTCGCCGATGTGATGAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTG 780
DB 721 ATGTCGCCGATGTGATGAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTG 780
QY 781 GCTTTGGCGTGGTGGACCAAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTG 840
DB 781 GCTTTGGCGTGGTGGACCAAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTG 840
QY 841 GTAGCCGAGGCTGTGAGAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTG 900
DB 841 GTAGCCGAGGCTGTGAGAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTGACAGGCTG 900
QY 901 CTTCTGAGCTCAAGCTGCGTTTATTAATGCTCTCTCCCGCAGGCGGCGGCGGCGGCGGCGGCT 960

DB 901 CTTCTGAGCTCAAGCTGCGTTTATTAATGCTCTCTCCCGCAGGCGGCGGCGGCGGCGGCT 960
QY 961 GCACAGATATTTCCATTTCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1020
DB 961 GCACAGATATTTCCATTTCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1020
QY 1021 TGAGTCTCTGCGGGAGTAGTTGGAAAGTTGGAACCGTGTCCAGCAGAGGAGGAAATCTGTG 1080
DB 1021 TGAGTCTCTGCGGGAGTAGTTGGAAAGTTGGAACCGTGTCCAGCAGAGGAGGAAATCTGTG 1080
QY 1081 CAGATGACGAGTGCACATGTTTACTTCCACGCGGAGGAGACGCTCAGAGGCGGCGGCGGCT 1140
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QY 1141 CGGAGCGAGGAGAGAGTGGAGAACTGGGATTTGAACCCCGCGCATCTCTTCCACGAGC 1200
DB 1141 CGGAGCGAGGAGAGAGTGGAGAACTGGGATTTGAACCCCGCGCATCTCTTCCACGAGC 1200
QY 1201 CCATGCTCAACCACTGTGGCGTTCTGCTCCCTGCGAGTTGGCAGAAAGGATGTTTTGT 1260
DB 1201 CCATGCTCAACCACTGTGGCGTTCTGCTCCCTGCGAGTTGGCAGAAAGGATGTTTTGT 1260
QY 1261 CCATTTCTTGGAGCGCCACCGGAGCAGACCTGGACACTGGACACTAGGGTTCAGGCGGCTGTG 1320
DB 1261 CCATTTCTTGGAGCGCCACCGGAGCAGACCTGGACACTAGGGTTCAGGCGGCTGTG 1320
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DB 1321 GTGGGAGGAGGATGCTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGG 1380
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DB 1381 TGGCCCTGTGAGTGTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGATGATGATGATGATG 1440
QY 1441 CCAGGAGAAATGAGATAATATCTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATG 1500
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DB 1621 AAAGCAGTCTCTTATTTCTGATAACAGAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
QY 1681 TACAAAAAATAAAAAA 1701
DB 1681 TACAAAAAATAAAAAA 1701

RESULT 3
PCT-US96-10521-1
; Sequence 1, Application PC/TUS9610521
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; NUMBER OF SEQUENCES: 34
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: PCT/US96/10521
; CLASSIFICATION:

US-09-064-414-1

Query Match						33.6%	Score	571.8	DB	4	Length	606
Best Local Similarity						96.3%	Pred.	No. 2	4e-121			
Matches						604	Conservative	0	Mismatches	2	Indels	21
						Gaps						
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QY	145	ATGGACCCGTTCTGTGTCGTGCTCACTCGGTGTCGTCCAGCCTGTGCAGCAGCGAGCTG	204									
Db	1	ATGGACCCGTTCTGTGTCGTGTCGACTCGGTGTCGTCCAGCCTGTGCAGCAGCGAGCTG	60									
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QY	205	ACCGAGCTCAAGTTCATATGCTCGGGGCGCGTGTCGAAGCGCAAGCTGGAGCGCGTGCAG	264									
Db	61	ACCGAGCTCAAGTTCATATGCTCGGGGCGCGTGTCGAAGCGCAAGCTGGAGCGCGTGCAG	120									
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QY	265	AGCGGCTTAGACTCTTCTCCATGCTGTGGAGCAGAACCCTGGAGCCCGGCCACACC	324									
Db	121	AGCGGCTTAGACTCTTCTCCATGCTGTGGAGCAGAACCCTGGAGCCCGGCCACACC	324									
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QY	325	GAGCTCTCTGCGGAGCTGCTCGCTCCCTGGGGCGCCACGACCTGCTCGCGCGCTCGAC	384									
Db	171	-----CGAGCTGCTCGCTCCCTGGGGCGCCACGACCTGCTCGCGCGCTCGAC	219									
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QY	385	GACTTCGAGCGGGGCGCGCGCGCGCTGGGAAGAAGACCTGTGTGTCAGCA	444									
Db	220	GACTTCGAGCGGGGCGCGCGCGCGCTGGGAAGAAGACCTGTGTGTCAGCA	279									
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QY	445	TTTAACGTCATATGTGATAATTGGGGAAGATTGGAGAAGGTGGTCTCATAGCTCAA	504									
Db	280	TTTAACGTCATATGTGATAATTGGGGAAGATTGGAGAAGGTGGTCTCATAGCTCAA	339									
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QY	505	GTCTCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCGCAACCTGCACAGACGT	564									
Db	340	GTCTCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCGCAACCTGCACAGACGT	399									
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QY	565	GTGGGGGAGTCACGTAGAATCTGGAAGAACACAGAAAGGAGAACCCACAGTGGCCCCAC	624									
Db	400	GTGGGGGAGTCACGTAGAATCTGGAAGAACACAGAAAGGAGAACCCACAGTGGCCCCAC	459									
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QY	625	CTGTTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGTT	684									
Db	460	CTGTTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGTT	519									
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QY	685	CAGCAGCCCGTGTACCTCCAACAGAGAGTGGGGCCATGTCCCAGTGTATCGGAATCA	744									
Db	520	CAGCAGCCCGTGTACCTCCAACAGAGAGTGGGGCCATGTCCCAGTGTATCGGAATCA	579									
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QY	745	GAGCATCTACCTCCGAAGCGTCCCTGA	771									
Db	580	GAGCATCTACCTCCGAAGCGTCCCTGA	606									

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RESULT      6
US-09-064-414-3
; Sequence 3, Application US/09064414
; Patent No. 6248875
; GENERAL INFORMATION:
; APPLICANT: Wood, Andrew T
; APPLICANT: Bingham, Brendan W
; APPLICANT: Young, Kathleen H
; APPLICANT: Birsan, Camella
; TITLE OF INVENTION: Neuronal MORF1 Isoforms
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Andrea C. Walsh
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 3:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..606
US-09-064-414-3

Query Match	33.5%	Score	570.2	DB 4	Length	606			
Best Local Similarity	96.3%	Pred. No.	5.5e-121						
Matches	603	Conservative	0	Mismatches	3	Indels	21	Gaps	
QY	145	ATGGACCGCTTCCCTGGTGTCTGCTGCTACTCGGTGTCTCTCAGGCTGTCTCAGGCTCTGTCAGGACGAGCTG	204						
Db	1	ATGGACCGCTTCCCTGGTGTCTGCTGCACTCGGTGTCTCTCAGGCTGTCTCAGGACGAGCTG	60						
QY	205	ACCGAGCTCAAGTTCCCTATGCCCTCGGCGCGTGGTCAAGCGCAAGCTGGAGCGCGTGCAG	264						
Db	61	ACCGAGCTCAAGTTCCCTATGCCCTCGGCGCGTGGCAAGCGCAAGCTGGAGCGCGTGCAG	130						
QY	265	ACGCGCCTAGACCTCTCTCTCCATGCTGTGGAGCAAGACGACCTGGAGCCCGGCGCACCC	324						
Db	121	ACGCGCCTAGACCTCTCTCTCCATGCTGTGGAGCAAGACGACCTGGAGCC	170						
QY	325	GAGCTCTCGCGGAGCTGTGCTCTCCCTCGCGGCCACGACACCTGCTGCGCGCGCTCGAC	384						
Db	171	-----CGAGCTGTCTGCTCTCCCTGCGGCCACGACCTGCTGCGCGCGTGCAC	219						
QY	385	GACTTCAGGCGGGGCGCGCGCGCGCTGCGGGAAGAACCTGTGTGCAGCA	444						
Db	220	GACTTCAGGCGGGGCGCGCGCGCGCTGCGGGAAGAACCTGTGTGCAGCA	279						
QY	445	TTTAACGCTCATATGTGATAATGTGGGGAAGATTGGAGAAGCGTGGCTCTGCTCAGCTCAAA	504						
Db	280	TTTAACGCTCATATGTGATAATGTGGGGAAGATTGGAGAAGCGTGGCTCTGCTCAGCTCAAA	339						
QY	505	GTCTTCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCAACCTGCAGAGCGT	564						
Db	340	GTCTCAGACACCAAGATCGACAGCATCGAGACAGATACCCCGCAACCTGCAGAGCGT	399						
QY	565	GTGGGAGTCACTGAGATCTGGAAGAACACAGAAAGAGAACGCAACAGTGGCCAC	624						
Db	400	GTGGGAGTCACTGAGATCTGGAAGAACACAGAAAGAGAACCAACAGTGGCCAC	459						
QY	625	CTGGTGGGGCTCTCAGTCTCTGCCAGATGAACCTGTGTGCTGACCTGGTACAGAGGTT	684						
Db	460	CTGGTGGGGCTCTCAGTCTCTGCCAGATGAACCTGGCGCTGACCTGGTACAAGAGTT	519						
QY	685	CAGCAGGCCGCTGACCTCCAGAACAGAGTGGGGCCATCTGCCGATGTCATGGAACTCA	744						
Db	520	CAGCAGGCCGCTGACCTCCAGAACAGAGTGGGGCCATCTGCCGATGTCATGGAACTCA	579						
QY	745	GACGCATCTACCTCGGAAGCGTCTCTGA	771						
Db	580	GACGCATCTACCTCGGAAGCGTCTCTGA	606						

RESULT 7

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US-09-335-409-1
; Sequence 1, Application US/09335409
; Patent No. 6121029
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/335,409
; CURRENT FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-335-409-1

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Query Match      3.1%; Score 52.6; DB 3; Length 68750;
Best Local Similarity 47.9%; Pred. No. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 109 GCCGGGCGGCAGCCCGCGCTTGCAGACCCCGCCATGGACCCGTTCTCTGGTGTGCTG 168
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Db 3985 ggcgcgtcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 169 CACTCGGTGTCTCCAGCCCTGTGACAGCGAGCTGACCGAGCTCAAGTTCTATGCCCTC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcatggctcgtcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
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QY 229 GGGCGCGTGTCAAGCGCAAGCTGGAGCGCGGCACACCGAGCTCCTGCGCGAGCTCGCC 288
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Db 4105 acgcgcgtctccaaaggacaggtgtcgtctcgtctcgtctcgtctcgtctcgtctcgt 288
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QY 289 CTGCTGGAGCAGAACGACTTGGAGCCCGGCACACCGAGCTCCTGCGCGAGCTCGCC 348
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QY 349 TCCTGCGCGCGCCAGCCTGTGCGCGCGCTGACGAGCTTCCAGTTCCTATGCCCTC 4224
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Db 4225 aacagcgcctctcgacccaaacccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 4224
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QY 409 GGGCGCGCGCTGGG 423
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Db 4285 ctcttcgcgcctgtg 4299
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RESULT 8
US-09-568-102-1
; Sequence 1, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,102
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750

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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-102-1

Query Match      3.1%; Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred. No. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 109 GCCGGGCGGCAGCCCGCGCTTGCAGACCCCGCCATGGACCCGTTCTCTGGTGTGCTG 168
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Db 3985 ggcgcgtcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 169 CACTCGGTGTCTCCAGCCCTGTGACAGCGAGCTGACCGAGCTCAAGTTCTATGCCCTC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcatggctcgtcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 229 GGGCGCGTGTCAAGCGCAAGCTGGAGCGCGGCACACCGAGCTCCTGCGCGAGCTCGCC 288
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Db 4105 acgcgcgtctccaaaggacaggtgtcgtctcgtctcgtctcgtctcgtctcgtctcgt 288
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QY 289 CTGCTGGAGCAGAACGACTTGGAGCCCGGCACACCGAGCTCCTGCGCGAGCTCGCC 348
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Db 4165 ctgacgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 348
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QY 349 TCCTGCGCGCGCCAGCCTGTGCGCGCGCTGACGAGCTTCCAGTTCCTATGCCCTC 4224
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Db 4225 aacagcgcctctcgacccaaacccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 4224
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QY 409 GGGCGCGCGCTGGG 423
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US-09-567-969-1
; Sequence 1, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-969-1

Query Match      3.1%; Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred. No. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 109 GCCGGGCGGCAGCCCGCGCTTGCAGACCCCGCCATGGACCCGTTCTCTGGTGTGCTG 168
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Db 3985 ggcgcgtcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 168
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QY 169 CACTCGGTGTCTCCAGCCCTGTGACAGCGAGCTGACCGAGCTCAAGTTCTATGCCCTC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcatggctcgtcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
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QY 229 GGGCGCGTGTCAAGCGCAAGCTGGAGCGCGGCACACCGAGCTCCTGCGCGAGCTCGCC 288
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; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
; US-09-568-472-1

Query Match          3.1%; Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred. NO. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 109 GCCGGCGCCGAGCGCGCTGTCAGAGCCCGCCATGACCCGCTCTCTGTCGTGCTG 168
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Db 3985 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 168
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QY 169 CACTCGGTGCTCCAGCTGTCGAGCAGCGAGCTGACCGAGCTCAAGTTCCTATGCCCTC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcattgctcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
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QY 229 GGCGCGGTGCTCAAGCGCAAGCTGGAGCGCTGTCAGAGCGGCTAGACCTCTTCCATG 288
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RESULT 13
US-07-642-734C-1
; Sequence 1, Application US/07642734C
; Patent No. 5824513
; GENERAL INFORMATION:
; APPLICANT: Katz, L
; APPLICANT: Donadio, S
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Recombinant DNA Method for Producing
; TITLE OF INVENTION: Erythromycin Analogs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edward H. Gorman
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Park Rd
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 17-JAN-91
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M
; REGISTRATION NUMBER: 32652
; REFERENCE/DOCKET NUMBER: 4952.US.01
; TELEPHONE: 708-937-9396
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11219 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: Saccharopolyspora erythraea
; STRAIN: NRRL 2338
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 00:40:30 ; Search time 220.39 seconds
(without alignments)
13251.379 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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2	1701	100.0	1701	18	AAT61397
3	1701	100.0	1701	21	AAZ44745
4	1621.8	95.3	1642	17	AAT30397
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6	620.6	36.5	627	20	AAV71930
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					MORT-1 coding sequ
					Human FADD DNA. H
					FADD (Fas-associat
					Human FADD protein
					MORT1 isoform MORT
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					Mouse apoptosis me

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	19	50.8	3.0	2842	21	AA000334
	20	50.8	3.0	2879	22	AA005820
	21	50.4	3.0	2561	22	AAH26500
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ALIGNMENTS

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XX AC AAT30372;
XX 13-SEP-1996 (first entry)
XX DE MORT-1 cDNA.
XX KW MORT-1; HFI; FAS/AP01 receptor; FAS-R; tumour; cancer; HIV;
XX KW mediator of receptor toxicity; gene therapy; ss.
XX OS Homo sapiens.
XX FH Key
XX CDS Location/Qualifiers
FT 1..771
FT /*tag= a
XX PN WO9618641-Al.
XX PD 20-JUN-1996.
XX PF 14-DEC-1995; 95WO-US16542.
XX PR 16-JUL-1995; 95IL-0114615.
XX PR 15-DEC-1994; 94IL-0112022.
XX PR 19-FEB-1995; 95IL-0112692.
XX PA (WEIN/) WEINWURZEL H.
XX PA (YEDA) YEDA RES & DEV CO LTD.

Human FADD mRNA.
Pseudomonas aerugin
Sorangium cellulos
Gene encoding a su
Human SNP oligonuc
Human OREF ORF1238
Human membrane as
Nucleotide sequenc
Rice raffinose syn
Human reproductive
Rabbit low density
Human DNA for pote
Human metalloprote
eryA region of S.
Human polynucleoti
Human cDNA encodin
Amycolatopsis medi
Metabotropic gluta
Micromonospora DNA
Fusaric acid reas
Protein PRO227 CDN
Human cDNA sequenc
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Total DNA sequence
S. aureofaciens DN
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Clone p8-2 encodin
cDNA encoding a su
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AAT61397
 ID AAT61397 standard; cDNA; 1701 BP.
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 AC AAT61397;
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 DT 29-OCT-1997 (first entry)
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 DE MORT-1 coding sequence.
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 KW MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death;
 KW antibody; FAS ligand receptor; FAS-R; death domain region; septic shock;
 KW tumour necrosis factor; tumour; HIV-infection; oligodendrocyte death;
 KW apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis;
 KW autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;
 KW TNF; therapy; ss.
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 OS Homo sapiens.
 OS
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 FT FT /*tag= a
 FT /product= mediator of cellular toxicity (MORT-1) protein
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 PN M09703998-A1.
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 PD
 PD 14-JUN-1996; 96WO-US10521.
 PF
 PR 16-APR-1996; 96IL-0117932.
 PR 17-JUL-1995; 95IL-0114615.
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 PR 27-SEP-1995; 95IL-0116588.
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 PA (WEIN/) WEINURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Boldin M, Goltsev YV, Goncharov T, Wallach D;
 XX
 XX WFI; 1997-132570/12.
 DR P-PSDB; AAW11894.
 XX
 XX New DNA encoding MACH protein that interacts with MORT-1 protein -
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.
 XX
 XX Disclosure; Page 102-103; 163pp; English.
 XX
 CC This sequence represents the coding sequence for the mediator of
 CC cellular toxicity (MORT-1) protein. The protein encoded by this sequence
 CC is bound by the protein of the invention (see AAW11892), designated MACH.
 CC MORT-1 binds to the FAS ligand receptor (FAS-R) death domain region, and
 CC triggers part of the cell death signalling cascade in mammalian cells.
 CC vectors containing MACH, the MACH protein, and antibodies (Ab) against
 CC it are used to modulate the effect of FAS-R ligand or TNF on cells that
 CC carry FAS-R or p55-R. This is specifically for treating tumours,
 CC HIV-infected cells or other diseased cells, by control of
 CC apoptosis/programmed cell death. The MACH protein is a mediator of the
 CC cell death pathway initiated by TNF and FAS-R binding, i.e. it mimics or
 CC enhances the effect of MORT-1 where increased cytotoxicity is required.
 CC To inhibit the effect of MORT-1, e.g. in cases of septic shock, graft
 CC rejection and acute hepatitis, sequences encoding antisense molecules or
 CC ribozymes, or Ab against MACH, are used. Compounds that inhibit MACH are
 CC potentially useful for controlling MACH activity e.g. in cases of
 CC autoimmune disease, oligodendrocyte death in multiple sclerosis or
 CC AIDS-inhibited T-cell suicide. The MACH protein can also be used to
 CC isolate and characterise other proteins and receptors involved in
 CC signalling and for Ab production. The Ab can be used to purify the new
 CC proteins and for diagnosis of conditions involving abnormal function of
 CC FAS-R mediated cellular effects.
 XX
 XX Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 other;

Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 other;

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XX AC AA244745;

XX AC AA244745;

DT 19-APR-2000 (first entry)

DE Human FADD DNA.

XX FADD; human; antisense; inhibitor; Fas-associated death domain; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 145..771

XX FT /*tag= a

XX FT /product= "FADD"

XX US6015712-A.

XX 18-JAN-2000.

XX

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PF 19-JUL-1999; 99US-0357072.
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PR 19-JUL-1999; 99US-0357072.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsett LM, Baker BF, Zhang H;
XX
DR WPI: 2000-126316/11.
DR P-PSDB; AAY51329.
XX
PT Antisense oligonucleotides, useful for inhibiting human Fas-associated
PT death domain (FADD) expression are targeted to the 3' untranslated
PT region of the FADD gene
XX
PS Example 13; Column 43-46; 37pp; English.
XX
CC This invention describes novel antisense oligonucleotides (OGNs) (I)
CC 8-20 nucleotides in length that specifically hybridize with and inhibit
CC nucleic acids encoding human Fas-associated death domain (FADD),
CC targeted to the 3' untranslated region (3'UTR). (I) can be used to treat
CC animals, especially humans, suspected of having or being prone to a
CC disease or condition associated with FADD expression. This sequence
CC encodes the human FADD protein described in the method of the invention.
XX
SQ Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 other;

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Query Match 100.0%; Score 1701; DB 21; Length 1701;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGAGACCTGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

Db 61 cgagacctggcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 120

QY 121 CCCGGCGCGCTGTGAGACCCCGCATGAGCCCGTCTCTGCTGTGCTGCTGCTGCTGCTG 180

Db 121 cccggcgctgtgagaccccgcatgagcccgctctctgctgtgctgctgctgctgctg 180

QY 181 TCCAGCTGTGAGCAGCAGCTGACCGAGCTCAAGTCTCTATGCTCTGCGCGCTGCTGCTG 240

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QY 541 TACCCCGCAACCTGACAGAGCTGTGGGGAGTCACTGAGAACTGGAAGAACACAGAG 600

Db 541 taccctcgcaacctgacagagcgtgtgaggagctcactgagaaactggaagacacagag 600

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Db 1321 gtgggagagcatgctggggtggggtgggagacctggtggccgtggtccagctct 1380
QY 1381 TGGCCCTGTGTGAGTTGAGTCTCTCTGAGACTGCTAGTAGGGCGAGTGATGTTG 1440
Db 1381 tggccctgtgtgagttgagctctctctctgagactgctagtagggcgagtgatggtg 1440
QY 1441 CCAGAGCAATTGAGATAATATCTGTGAGTGTCTGATGAGTGTGATGACACAGCACTCT 1500
Db 1441 ccagagcaattgagataatatctgtgagtgctgagtgatgattgacacacagcactct 1500
QY 1501 CTAAATCTCTCTGAGGATTATGGTCTCTGCAATTTCTACAGTTTCTTACTGTTTGA 1560
Db 1501 ctaaactctctctgaggattatgggtctctgcaatttctacagtttcttactgtttgta 1560
QY 1561 TCAAAATCACTATCTTCTGATACAGAATTTGCCAAGCGAGCGGATCTCGTATCTTAA 1620
Db 1561 tcaaaatcactatcttctgataacagaaatgccaagggcagcggtatctgtatcttaa 1620
QY 1621 AAAGCAGTCTCTTATTCCTAAGTAATCTTATTAACACAGCTTTTACAACTTCCATAT 1680
Db 1621 aaagcagctctcttattctcctaagtaattcttataaacaacagcttttacaacttccat 1680
QY 1681 TACAAAAAATAAAAAA 1701
|||||
```

Db 1681 tacaaaaaaaaaaaaaaaa 1701

RESULT 4
AAT39397
ID AAT39397 standard; CDNA; 1642 BP.
XX AAT39397;
AC AAT39397;
XX 22-FEB-1997 (first entry)
XX FADD (Fas-associating protein with novel death domain) gene.
XX Human; FADD; Fas-associating protein with novel death domain;
XX apoptosis; Fas receptor; death domain; gene therapy; antibody;
XX immunosay; drug screening; diagnostic; AIDS; antiinflammatory;
XX antitumour; cerebroprotective; neuroprotective; ss.
XX Homo sapiens.
XX Key
XX 5'UTR
XX Location/Qualifiers
XX 1..129
XX /tag= a
XX misc_feature
XX 4..6
XX /tag= b
XX /note= "In-frame stop codon"
XX CDS
XX 130..756
XX /tag= c
XX /product= FADD protein
XX 133..501
XX /tag= d
XX /note= "Encodes N-terminal half, inducing apoptosis
XX but not binding Fas receptor"
XX misc_feature
XX 198
XX /tag= e
XX /note= "Clone 15 start point"
XX 249
XX /tag= f
XX /note= "Clone 8 start point"
XX misc_feature
XX 460..660
XX /tag= g
XX /note= "Region encoding death domain"
XX 757..1642
XX /tag= h
XX polyA_signal
XX 1636..1641
XX /tag= i
XX WO9631603-A2.
XX
XX
XX 10-OCT-1996.
XX
XX 28-FEB-1996; 96WO-US02857.
XX
XX 18-MAY-1995; 95US-0443982.
XX 03-APR-1995; 95US-0416379.
XX (UNMI) UNIV MICHIGAN.
XX
XX Dixit VM, O'Rourke K;
XX WPI: 1996-465026/46.
XX P-PSDB; AAW03653.
XX
XX FADD protein that binds to cytoplasmic region of Fas receptor - for
XX identifying inhibitors of Fas-associated apoptosis useful for
XX treating e.g. AIDS, leukaemia, stroke, etc
XX
XX Example 1; Fig 2A-B; 96pp; English.
XX
XX The sequence encodes FADD (Fas-associating protein with novel death
XX domain), which binds the cytoplasmic region of a Fas receptor, and
XX modulates apoptosis induced by activation of the receptor by ligand
XX binding. The cDNA has been isolated using a yeast two-hybrid system


```
Oy 563 GTGTGGGGAGTCACTGAGAACTCTGGAACACACAGAGAGGAGAACGACAGTGGGCC 622
   || || || || || || || || || || || || || || || || || || || || ||
Db 431 gggtaaggagagtgctgaagctgaaagatgctgagaagaagacgcctcggtggccg 490
   || || || || || || || || || || || || || || || || || || || || ||
Oy 623 ACCGTGGTGGGGCTCTCAGGTCCTCCAGATCAACCTGGTGGCTGACCTGGTACAGAGG 682
   || || || || || || || || || || || || || || || || || || || || ||
Db 491 gactggtcaaggcgtcggaacgtcaggctgaatctggtgctgacctggtggaag--- 547
   || || || || || || || || || || || || || || || || || || || || ||
Oy 683 TTCACGAGCGCGCTCACCTCCACAGACAGAGTGGGCCATGTCCTCCGATGTCATGGAAC 742
   || || || || || || || || || || || || || || || || || || || || ||
Db 548 -----agccaggaaatctgagcagagtgagaatatgcccagctactaaggatt 601
   || || || || || || || || || || || || || || || || || || || || ||
Oy 743 CAGAGCGCATCTACCTCCGAAGCGTCTGATGGGCC 777
   || || || || || || || || || || || || || || || || || || || || ||
Db 602 caactgtgtcttcctcagaaacacacctgacaagcc 636
   || || || || || || || || || || || || || || || || || || || || ||

RESULT 10
AAF90364
ID AAF90364 standard; mRNA; 298 BP.
AC AAF90364;
XX
DT 06-AUG-2001 (first entry)
DE Human FADD mRNA.
KW FADD; Fas-associated death domain; human; ribozyme; gene therapy;
KW apoptosis; antiapoptotic; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 158..159
   /tag= a
   /note= "cleavage site of ribozyme FADD-Rz1"
FT misc_feature 167..168
   /tag= b
   /note= "cleavage site of ribozyme FADD-Rz2"
FT misc_feature 176..177
   /tag= c
   /note= "cleavage site of ribozyme FADD-Rz3"
FT misc_feature 264..265
   /tag= d
   /note= "cleavage site of ribozyme FADD-Rz4"
XX
PN EP1097993-A2.
XX
PD 09-MAY-2001.
XX
PF 03-NOV-2000; 2000EP-0250368.
XX
PR 05-NOV-1999; 99JP-0316133.
XX
PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
PA (TAIR/) TAIRA K.
XX
PI Taiza K, Warashina M, Kuwabara T, Kawasaki H;
XX
DR WPI; 2001-357832/38.
XX
PT Novel chimeric molecule useful for clarifying biological function of
PT target nucleic acid and for treating viral diseases, and Alzheimer's
PT disease, comprises region with binding affinity for molecule capable of
PT sliding -
XX
XX Example 3; Fig 13C; 76pp; English.
XX
PS The present sequence is that of the 5' region of mRNA of human
CC pro-apoptotic factor FADD (Fas-associated death domain). The
CC invention provides 4 polyA-linked and -nonlinked ribozymes (see
CC AAF90365, AAF90367, AAF90369, AAF90371) aimed at specific sites
CC in this mRNA. Ribozymes FADD-Rz1, -Rz2 and -Rz3 were designed to
```

```
CC target inaccessible sites located in a stable stem structure,
CC while ribozyme FADD-Rz4 was designed, as a control, to target a
CC relatively accessible site located in a loop region of the FADD
CC mRNA. The ribozymes were cloned into parental trNAval-expression
CC vector pUCdT. Addition of the polyA sequence to the ribozymes
CC allowed recruitment of eIF4A1 RNA helicase, which coupled the
CC unwinding activity of the helicase to the cleavage activity of
CC the ribozymes. This facilitated cleavage of RNA previously
CC refractory to cleavage because of its high-order structure.
CC Chimeric molecules of the invention, including polyA-linked
CC ribozymes, or expression vectors, are used to prevent or treat
CC viral diseases, diseases associated with apoptosis or diseases
CC associated with abnormal gene expression (claimed). They are also
CC used in a claimed method of specifically cleaving a target nucleic
CC acid, especially a viral gene, protooncogene or a gene associated
CC with apoptosis.
XX
SQ Sequence 298 BP; 49 A; 96 C; 109 G; 44 U; 0 other;
```

```
Query Match 17.0%; Score 288.8; DB 22; Length 298;
Best Local Similarity 84.9%; Pred. No. 5.6e-56;
Matches 248; Conservative 42; Mismatches 2; Indels 0; Gaps 0;
Oy 22 AGTTTCGGGGTGAATCTTGGCCGCTGGCGCAAGCGCGAGACCTGGCCAGGCCACG 81
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 7 agguucgggggugauucucugggcgucgggcaagcgcgagaccgagggccagc 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 82 GAGCGAGGACAGAGGGCGCGGAGGGCGGCGCGAGCGCGCGCGCTTCGACAGCC 141
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 67 gagcgaggagagggcgacgagggcgggcgccgcccgcgucgucgagacc 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 142 GCATGGACCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 gcauaggaccgcuucucugugugucgucgacucgugucgucgagcagcgag 186
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 202 CTGACCGAGCTCAAGTCTCTATGCTGCGGCGCGTGTCAACGCGAGCTGGAGCG 261
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 cugaccgagcucauguucuaugcucggcgcgugggcgagcgcaagcugagcgug 246
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 262 CAGAGCGGCTAGACCTCTTCTCCATGCTGCTGGAGCAGACAGACCTGGAGC 313
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 247 cagagcgccagacucucuccaugcuguggagcgagcagaccugagc 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 11
AAS54123/c
ID AAS54123 standard; DNA; 1611 BP.
XX
AC AAS54123;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #254.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-20727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
```


[illegible]

complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections

Claim 1; Page 2843; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 51 BP; 14 A; 11 C; 19 G; 7 T; 0 other;

Query Match 3.0%; Score 51; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 TCCGCGACACGCGCGGCTTGGCCCTGCACAGATATTTCCATTTCTCCT 984
|||||
Db 51 TCCGCGACACGCGCGGCTTGGCCCTGCACAGATATTTCCATTTCTCCT 1

RESULT 15
AAC75683
ID AAC75683 standard; cDNA; 1251 BP.
XX
AC AAC75683;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF1238 polynucleotide sequence SEQ ID NO:2475.
XX
KW Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;
KW vulnerable; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

9551 asyathrsrscysaagxtraasraaargashhargsgysysgrscrcysysrvagy 9610
QY 493 CGTCAGCTCAAGTCTCAACACACAGATCGACAGATCGACAGACATACCCCGGCAAC 552
Db 9611 aasrasasmtaashvagmtgysaavavasarvagysaathrgnsrrraasysaavat 9670
QY 553 CTGACAGAGCGGTGCGGGAGTCACTGAGAAATCTGGAGAACACAGAGAGAGAGCA 612
Db 9671 hrgasnsrgrgthrythrysgsrthrggyysgrvarashsgrntrthrgthrthr 9730
QY 613 ACAGTGGCCACCTGGTGGGGCTCTCAGTCTGCTCCAGATGAACCTGGTGGCTGACCTG 672
Db 9731 rgvavaasmtgrmtsrashsrasyssrasyasnthrcysrshsrygthrvargytr 9790
QY 673 GTACAAGAGTTACAGAGCGCGTCACTCCAGAACAGAGAGTGGCCATGTCCCGCATG 732
Db 9791 gnasvavaysthrgnasnshvathrshsyrasasasysvaaaahghsaaasnas 9850
QY 733 TCATGGAACTCAGACGATCTACCTCCGAGCGTCTGTAGTGGCGCGTCTGCTCGGTGG 792
Db 9851 ashshasrsrargysrvahsa-----sthrgnasnrrgncysrshscysrcy 9899
QY 793 TGGACACAGGCATCTACAGCGCTGACITTTGTTCTCCAGGAAGGTAGCCACGAC 852
Db 9900 srasrsrvavaasnraraagygasnaasasrsyarsgrgrngasrsysrsgysgva 9959
QY 853 TGTGAAGACCCAGGAGCCAGGCTGAGTGAGCCACACACACCTGCTTCTCAACTCA 912
Db 9960 gargaavaasatycasarsraargysgyvargashartyasasngymtrthrgtyr 10019
QY 913 AGCTGCGTTTAAATGCTCTCCGNCACAGCGCGGCTTGGCCCTGCACAGATATTT 972
Db 10020 mtvaargvahgntyrsthrsrgrsyvaghshvacystyrasrgyysthrasatryga 10079
QY 973 CCATTTCTCTCACTATGACACTGAGCAAGATCTGTCTCCACTAAATGAGTCTCTCGC 1032
Db 10080 snhaegyChrthraaastmtashhscysrshrgnasvasrsmrtargasaasysgshas 10139
QY 1033 GGAGTAGTTGGAAGTTGGACCGTGTCCAGCACAGAGGAATCTGTGCAGATGAGCAGT 1092
Db 10140 trasgthrgasrgasgygaasngthrvavagysgarghsrargasnsrstrgnvathr 10199
QY 1093 CACACTGTACTC-CACAGCGGAGAGACACAGCTCAGAGGCCAGGATCGGAGCGAAGC 1151
Db 10200 hrrscysghasngasngygytrrasngysghtrasyasysrsgasrsgysgva 10259
QY 1152 AGAGAGGTGGAGACTGGGATTTGAACCCCGCCATCTCCACAGAGCCCATGCTCAAC 1211
Db 10260 garysgnsraathrasarggsmrtasngngsrgysthrasrarggnsrhygsra 10319
QY 1212 CACTGTGCGTCTCTGCTCCCTGAGTTGGCAGAAAGATGTTTTGTCCCATTTCTCTT 1271
Db 10320 sngyngasngysaasngysaasnasngnshthrgaagysaaaahsasnyavahr 10379
QY 1272 GGAGGCCACCGGACAGACCTGACACTAGGTGAGCGGGGTGCTGTTGGGGAG 1328
Db 10380 gggaasnasraancysgggaayscysggngngsrmtrsyrgcysrshsasas 10436

RESULT 14
AAL31857/c
ID AAL31857 standard; DNA; 51 BP.
XX
AC AAL31857;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5065.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

